

### **III. Rejection of Claims Under 35 U.S.C. § 112, First Paragraph**

The Action rejects claims 1-8 under 35 U.S.C. § 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention. Applicants respectfully submit that as claims 1-8 have been shown to have “a specific, substantial, and credible utility” as detailed in the section below. Applicants therefore request that the rejection of claims 1-8 under 35 U.S.C. § 112, first paragraph, be withdrawn.

### **IV. Rejection of Claims Under 35 U.S.C. § 101**

The Action next rejects claims 1-8 under 35 U.S.C. § 101, because the claimed invention lacks patentable utility for the reasons stated in the previous Office Action. Applicants respectfully traverse.

The Action seems to be implying that the use of the abbreviation NHPs, for novel human proteins is indicative of a lack of understanding or knowledge on the part of Appellant. Appellants are unaware of any regulation requiring the particular naming of a claimed sequence in order for the sequence to meet the utility requirements. Second, the Examiner also seems to be implying that because Appellants’ sequence is novel, it lacks utility. Appellants are unaware of any patent law, patent rule, or ruling from the Supreme Court or the Court of Appeals for the Federal Circuit that supports this untenable position.

The Action argues in section (i) that the present invention lacks real world utility. Applicants respectfully disagree. As taught in the application and as well known to those of skill in the art, G protein coupled receptors (GPCRs) play a critical role in, *intra alia*, signal transduction and cell activation. In fact, many oncogenes are linked to GPCRs. In addition, GPCRs are, as evidenced by Gurrath (Current Medicinal Chemistry, 8, 1605-1648, 2001: **Exhibit C**), prominent drug targets and approximately 60% of marketed prescription drugs are directed at this signal transduction system. Therefore, Applicants submit that the identification of a new and novel human GPCRs have a well recognized utility to those of skill in the art.

The Action also argues (in sections (ii) and (iii), pages 5 and 6), that applicants argument of due process presented in Paper No. 10 is not persuasive. Applicants understanding is that issued United States patents retain a legal presumption of validity which in this case indicates that the inventions

claimed in the cited patents are *legally presumed* to be in full compliance with the provisions of 35 U.S.C. sections 101, 102, 103, and 112. Applicants respectfully submit that, absent a change in the law as enacted by Congress and signed by the President, it is improper for the Examiner to hold Applicants' invention to a different legal standard of patentability. Given the rapid pace of development in the biotechnology arts, it is difficult for the Applicants to understand how an invention fully disclosed and free of prior art at the time the present application was filed, could somehow retain *less* utility and be *less* enabled than inventions in the cited issued U.S. patents (which were filed during a time when the level of skill in the art was clearly lower). Simply put, Applicants invention is *more* enabled and retains *at least as much* utility as the inventions described in the claims of the U.S. patents of record. Any argument to the contrary is at best arbitrary and at worst capricious. Absent authority provided by an act of Congress or Executive order, arbitrary or capricious conduct by an administrative office the U.S. government has historically proven to conflict with the provisions of the U.S. Constitution. The Patent Office does not have the authority to rewrite U.S. law. However, the Patent Office does have a Constitutional obligation to administer U.S. law in an unbiased and procedurally consistent manner. That is what the Applicants are respectfully requesting the Examiner to consider in the present matter.

The Action also disagrees, in section (iv), that Applicants assertion based on the evidence that the identical protein was identified by those of skill in the art in no way associated with Applicant indicates that Applicants assertions are credible. Given the legal test for utility simply involves an assessment of whether those skilled in the art would find any of the utilities described for the invention to be credible or believable, this is clear evidence that those skilled in the art would have recognized the function and activity of the protein encoded by the sequences of the present invention, there can, therefore, be no question that Applicants' asserted utility for the described sequences is "credible." As the human olfactory receptor 2B6, such a NGPCR would be recognized by those of skill in the art as having particular utility for its biological role and as a drug target. Agonists and antagonists directed at this NGPCR could effect feeding behavior and thus potentially address, *inter alia*, obesity, anorexia or cachexia and other feeding disorders. Molecules increasing or decreasing the activity of this NGPCR could also effect an individuals response to pheromones, thus treating sexual disorders through its effect on perceived attractiveness.

The Action states that "Applicant asserts that the NGPCR protein (SEQ ID NO:2) of the

instant invention is homologous to existing G protein coupled receptors, specifically odorant receptors”(page 7, lines 17-18) and the Action quotes an article by Ji *et al.* (“Ji”; 1998, J. Biol. Chem. 273:17299-17302), as teaching that structural homology alone is not a good predictor of function. But an exact quote from Ji completely undermines this argument: “a substantial degree of amino acid homology is found between members of a particular subfamily, but comparisons between subfamilies show significantly less or no similarity” (Ji at 17299, first paragraph, emphasis added). This quote suggests that homology with members of a G-protein coupled receptor is indicative that the particular sequence is in fact a member of that subfamily - the fact that there is little or no homology between subfamilies is completely irrelevant.

The Action also suggests that the use of the presently claimed polynucleotides, as in DNA chips, would be generic (section (v), page 10). Further, the Action seems to be requiring Applicants to identify the biological role of the nucleic acid or function of the protein encoded by the presently claimed polynucleotides before the present sequences can be used in gene chip applications that meet the requirements of § 101. Applicants respectfully point out that knowledge of the exact function or role of the presently claimed sequence is not required to track expression patterns using a DNA chip. As set forth in Applicants First Response, given the widespread utility of such “gene chip” methods using *public domain* gene sequence information, there can be little doubt that the use of the presently described *novel* sequences would have great utility in such DNA chip applications. The claimed sequence provides a specific marker of the human genome (see evidence below), and that such specific markers are targets for discovering drugs that are associated with human disease. Thus, those skilled in the art would instantly recognize that the present nucleotide sequence would be an ideal, novel candidate for assessing gene expression using, for example, DNA chips, as the specification details at least on page 9. Such “DNA chips” clearly have utility, as evidenced by hundreds of issued U.S. Patents, as exemplified by U.S. Patent Nos. 5,445,934, 5,556,752, 5,744,305, as well as more recently issued U.S. Patent Nos. 5,837,832, 6,156,501 and 6,261,776. Accordingly, the present sequence has a specific utility in such DNA chip applications. Clearly, compositions that enhance the utility of such DNA chips, such as the presently claimed nucleotide sequence, must also be useful.

Additionally, since only a small percentage of the genome (2-4%) actually encodes exons, which in-turn encode amino acid sequences. Thus, not all human genomic DNA sequences are useful

in such gene chip applications, further discounting the Examiner's position that such uses are "generic". Thus, the present claims clearly meet the requirements of 35 U.S.C. § 101. It has been clearly established that a statement of utility in a specification must be accepted absent reasons why one skilled in the art would have reason to doubt the objective truth of such statement. *In re Langer*, 503 F.2d 1380, 1391, 183 USPQ 288, 297 (CCPA, 1974); *In re Marzocchi*, 439 F.2d 220, 224, 169 USPQ 367, 370 (CCPA, 1971).

Evidence of the "real world" substantial utility of the present invention is further provided by the fact that there is an entire industry established based on the use of gene sequences or fragments thereof in a gene chip format. Perhaps the most notable gene chip company is Affymetrix. However, there are many companies which have, at one time or another, concentrated on the use of gene sequences or fragments, in gene chip and non-gene chip formats, for example: Gene Logic, ABI-Perkin-Elmer, HySeq and Incyte. In addition, one such company, Rosetta Inpharmatics, was viewed to have such "real world" value that it was acquired by large pharmaceutical company, Merck & Co., for substantial sums of money (net equity value of the transaction was \$620 million). The "real world" substantial industrial utility of gene sequences or fragments would, therefore, appear to be widespread and well established. Clearly, persons of skill in the art, as well as venture capitalists and investors, readily recognize the utility, both scientific and commercial, of genomic data in general, and specifically human genomic data. Billions of dollars have been invested in the human genome project, resulting in useful genomic data (see, e.g., Venter *et al.*, 2001, Science 291:1304). The results have been a stunning success as the utility of human genomic data has been widely recognized as a great gift to humanity (see, e.g., Jasny and Kennedy, 2001, Science 291:1153). Clearly, the usefulness of human genomic data, such as the presently claimed nucleic acid molecules, is substantial and credible (worthy of billions of dollars and the creation of numerous companies focused on such information) and well-established (the utility of human genomic information has been clearly understood for many years).

Further evidence of utility of the presently claimed polynucleotide, although only one is needed to meet the requirements of 35 U.S.C. § 101 (*Raytheon v. Roper*, 220 USPQ 592 (Fed. Cir. 1983); *In re Gottlieb*, 140 USPQ 665 (CCPA 1964); *In re Malachowski*, 189 USPQ 432 (CCPA 1976); *Hoffman v. Klaus*, 9 USPQ2d 1657 (Bd. Pat. App. & Inter. 1988)), is the utility the present nucleotide sequence has a specific utility in determining the genomic structure of the corresponding

human chromosome, for example mapping the protein encoding regions, as described in the specification at least at page 14, line 1 and evidenced below. Clearly, the present polynucleotide provides exquisite specificity in localizing the specific region of the human chromosome containing the gene encoding the given polynucleotide, a utility not shared by virtually any other nucleic acid sequences (see evidence below). In fact, it is this specificity that makes this particular sequence so useful. Early gene mapping techniques relied on methods such as Giemsa staining to identify regions of chromosomes. However, such techniques produced genetic maps with a resolution of only 5 to 10 megabases, far too low to be of much help in identifying specific genes involved in disease. The skilled artisan readily appreciates the significant benefit afforded by markers that map a specific locus of the human genome, such as the present nucleic acid sequence.

Only a minor percentage of the genome actually encodes exons, which in-turn encode amino acid sequences. The presently claimed polynucleotide sequence provides biologically validated empirical data (*e.g.*, showing which sequences are transcribed, spliced, and polyadenylated) that *specifically* define that portion of the corresponding genomic locus that actually encodes exon sequence. Equally significant is that the claimed polynucleotide sequence defines how the encoded exons are actually spliced together to produce an active transcript (*i.e.*, the described sequences are useful for functionally defining exon splice-junctions). The Applicants respectfully submit that the practical scientific value of expressed, spliced, and polyadenylated mRNA sequences is readily apparent to those skilled in the relevant biological and biochemical arts. For further evidence in support of the Applicants' position, the Board is requested to review, for example, section 3 of Venter *et al.* (*supra* at pp. 1317-1321, including Fig. 11 at pp.1324-1325), which demonstrates the significance of expressed sequence information in the structural analysis of genomic data. The presently claimed polynucleotide sequence defines a biologically validated sequence that provides a unique and specific resource for mapping the genome essentially as described in the Venter *et al.* article.

As evidence of the specific utility of the sequences of the present invention in localizing the specific region of the human chromosome and identification of functionally active intron/exon splice junctions is the information provided in **Exhibit D**. A blast analysis using the SEQ ID NO:1 of the present invention indicates that the coding the sequence is present on chromosome 6 and contained within clone AL133267.

For each of the foregoing reasons, Applicants submit that in light of the above discussion and those presented in Paper No. 10, the presently claimed invention has been shown to have a substantial, specific, credible and well-established utility and that the rejection of pending claims 2-8 under 35 U.S.C. § 101 has been avoided, and respectfully request that the rejection be withdrawn.

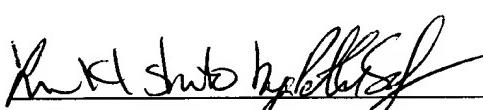
**V. Conclusion**

The present document is a full and complete response to the Final Office Action. In conclusion, Applicants submit that, in light of the foregoing remarks, the present case is in condition for allowance, and such favorable action is respectfully requested. Should Examiner Bunner have any questions or comments, or believe that certain amendments of the claims might serve to improve their clarity, a telephone call to the undersigned Applicants' representative is earnestly solicited.

Respectfully submitted,

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PATENT TRADEMARK OFFICE

**Exhibit A**

**Clean Version of The Pending Claims in U.S. Patent Application Ser. No. 09/755,017**

2. (Amended) An isolated nucleic acid molecule comprising a sequence that:

- (a) encodes at least fifty contiguous amino acids of the amino acid sequence of SEQ ID NO: 2; and
- (b) hybridizes under stringent conditions with wash conditions of 0.1xSSC/0.1% SDS at 68°C to the nucleotide sequence of SEQ ID NO: 1 or the complement thereof.

3. An isolated nucleic acid molecule comprising the nucleic acid sequence presented in SEQ ID NO: 1.

4. An isolated nucleic acid molecule comprising a nucleotide sequence that encodes the amino acid sequence shown in SEQ ID NO: 2.

5. (Amended) A recombinant expression vector comprising the nucleic acid molecule of claim 3.

6. (New) A host cell comprising the recombinant expression vector of claim 5.

7. (Amended) A recombinant expression vector comprising the nucleic acid molecule of claim 4.

8. (New) A host cell comprising the recombinant expression vector of claim 7.

**Exhibit B**

**Marked Up Version of Amended Claims in U.S. Patent Application Ser. No. 09/755,107**

1. (Cancelled) An isolated nucleic acid molecule comprising at least 80 contiguous bases of the nucleotide sequence described in SEQ ID NO: 1.
2. (Amended) An isolated nucleic acid molecule comprising a sequence that:
  - (a) encodes at least fifty contiguous amino acids of the amino acid sequence of SEQ ID NO: 2; and
  - (b) hybridizes under stringent conditions with wash conditions of 0.1xSSC/0.1% SDS at 68°C to the nucleotide sequence of SEQ ID NO: 1 or the complement thereof.
3. An isolated nucleic acid molecule comprising the nucleic acid sequence presented in SEQ ID NO: 1.
4. An isolated nucleic acid molecule comprising a nucleotide sequence that encodes the amino acid sequence shown in SEQ ID NO: 2.
5. (Amended) A recombinant expression vector comprising the [isolated] nucleic acid molecule of claim [1] 3.
6. (New) A host cell comprising the recombinant expression vector of claim 5.
7. (Amended) A recombinant expression vector comprising the [isolated] nucleic acid molecule of claim 4.
8. (New) A host cell comprising the recombinant expression vector of claim 7.

# Peptide-Binding G Protein-Coupled Receptors: New Opportunities for Drug Design

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**Abstract:** Over the last decades distinct members of the G Protein-Coupled Receptor (GPCR) family emerged as prominent drug targets within pharmaceutical research, since approximately 60 % of marketed prescription drugs act by selectively addressing representatives of that class of transmembrane signal transduction systems. It is noteworthy that the majority of GPCR-targeted drugs elicit their biological activity by selective agonism or antagonism of biogenic monoamine receptors, while the development status of peptide-binding GPCR-addressing compounds is still in its infancy.



Exemplified on selected medicinal chemistry projects, this review will focus on the opportunities of therapeutic intervention into a broad spectrum of disease processes through agonizing or antagonizing the functions of peptide-binding GPCRs. In this context, a brief overview of GPCR-mediated signal transduction pathways will be given in order to emphasize the biomedical relevance of a controlled modulation of receptor function. Modern trends on lead finding and optimization strategies for peptide-binding GPCR-targeted low-molecular weight compounds will be highlighted on the basis of current research programs conducted in the areas of angiotensin II, endothelin, bradykinin, neurokinin, neuropeptide Y, LHRH, C5a antagonists, and somatostatin agonists, respectively. Special emphasis will be laid on the elaboration and utilization of structural rationales on the potential drug candidates, thus facilitating more detailed insights into the underlying molecular recognition event.

## INTRODUCTION

Current pharmaceutical research is going through a period of unprecedented change, since new revolutionizing techniques have been successfully implemented into the pharmaceutical discovery process. At the same time, pharmaceutical industry feels growing pressure to release more new chemical entities (NCEs) that evolve as highly selective drugs targeting therapeutic areas of unmet medical need and address novel mechanisms of action. These attributes clearly define an ideal set of preconditions for positioning a candidate with block buster potential onto the drug market [1-3]. The conceptual combination of automated combinatorial chemistry, multiple parallel synthesis with high-throughput screening has dramatically altered the process of lead finding in medicinal chemistry in that vast numbers of low molecular weight compounds can rapidly be screened against biological target systems [4]. This progress in medicinal chemistry is paralleled on the side of target identification and validation with the maturation of genomics, proteomics, and bioinformatics in pharmaceutical research [5]. Taken together, these novel methodologies are expected to facilitate and accelerate the overall drug discovery process significantly.

However, the judicious choice of a disease relevant target is still one of the most crucial steps in initiating a drug

discovery project, both in terms of novelty and uniqueness of the underlying therapeutic principle, as well as the competitor situation [2].

In this context, the superfamily of transmembrane G protein-coupled receptors (GPCRs) emerged as the most prominent class of qualified drug targets for pharmaceutical research and biomedical application [6]. Approximately 60% of all commercially available drugs work by selective modulation of distinct members of this target family [7]. Even though an estimated number of 1000 to 2000 GPCRs is expected to exist in the human genome [8], current GPCR-targeted therapeutic principles exploit a surprisingly small fraction of the GPCR family known today. A strong bias exists among the GPCR-targeted drugs in favour of the subclass of biogenic monoamine-stimulated GPCRs, i.e. the classical neurotransmitter-binding receptors [9,10].

This review will focus on the opportunity to further expand the spectrum of drug-targeted GPCRs onto the huge subclass of peptide-binding representatives of that target family. After a brief introduction on the basic principles of receptor structure and function, the chemically diverse set of endogenous ligands will be discussed with the aim to emphasize the relevance of peptide-binding GPCRs for modern drug discovery.

The lead identification and optimization attempts discussed in this contribution are restricted on projects that are aimed to identify peptidomimetic or non-peptide agonists or antagonists. Numerous pharmaceutical research efforts conducted over the last two decades have clearly proven the

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relevance of an early pharmacokinetic profiling. Consequently, satisfactory metabolic stability and oral bioavailability demand a transfer of the peptide-encoded biological and structural information onto non-peptide, drug-like scaffolds in order to achieve the desired goal [11-13].

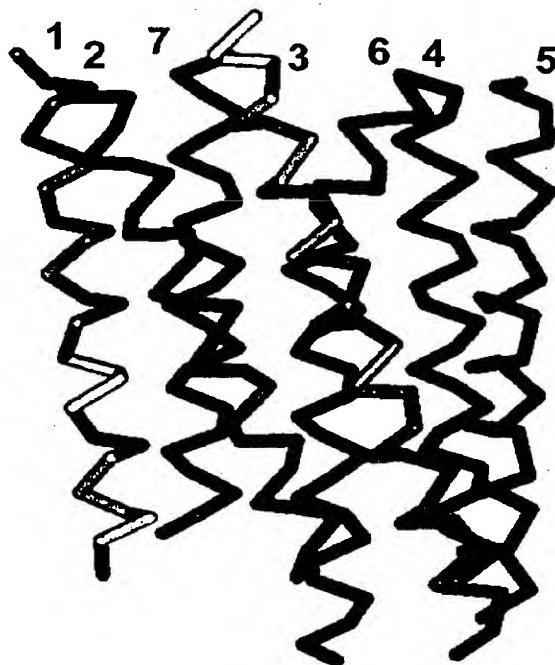
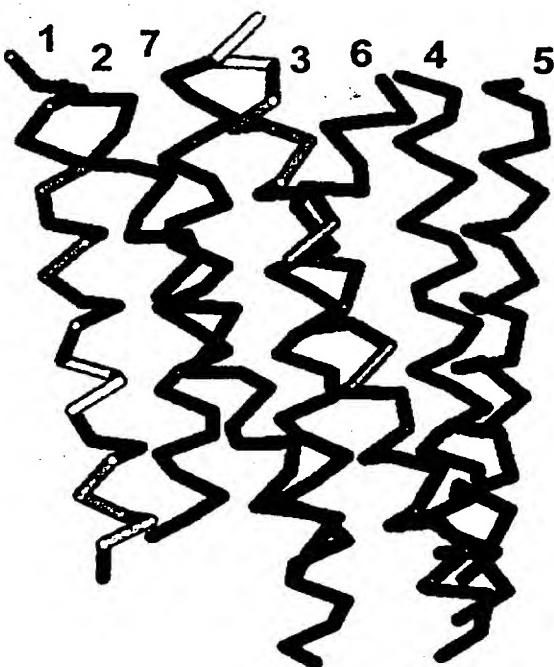
Classical attempts towards drugs selectively addressing peptide-binding GPCRs will be exemplified on the angiotensin II and endothelin receptor antagonists. In both areas, leads were identified by screening programs and further optimized by classical medicinal chemistry approaches to yield clinical candidates, some of which already entered the market. The classical approach of optimizing screening hits will further be introduced with medicinal chemistry programs aimed to identify active compounds for a modulation of the bradykinin, neurokinin, and NPY (neuropeptide Y) receptors. Since the area of peptide-binding GPCR compounds is still in its infancy, especially when compared to the situation of biogenic amine-binding receptor drugs, the actual state of the majority of projects discussed in this review is still in the preclinical or in early clinical phases. Apart from random lead finding attempts, structural rationales are more frequently used in recent times, preceded by studies on somatostatin, bradykinin, neurokinin, LHRH (luteinizing hormone-releasing hormone), and anaphylatoxin C5a receptor agonists and antagonists that will be discussed briefly. Structural rationales were mainly derived from an educated guess on the bioactive conformation of the endogenous peptide or protein ligand, thus offering the opportunity to follow an indirect drug design approach.

## GPCR SUPERFAMILY

G protein-coupled receptors constitute the largest receptor family known today [8]. According to an analysis of the *C. elegans* genome [14], approximately 5% of the 19100 nematode genes encode GPCRs with a family distribution profile that is reminiscent to that of mammalian GPCR genes. Extrapolation of these findings would suggest that up to 5000 distinct GPCR-encoding genes exist within the human genome (5% of an estimated 100000 genes). Currently, more than 800 distinct members of the GPCR superfamily have been cloned from various species, ranging from fungi over plants, yeast, slime mould, protozoa, metazoa to humans. Apart from the sensory olfactory receptors, approximately 150 human GPCRs have been cloned for which also the endogenous ligands have been identified. Further, more than 100 GPCRs are known with unidentified ligands and unknown physiological relevance, so called orphan GPCRs, which undoubtedly represent a rich source of disease-relevant drug targets for future biomedical research [15-17].

## Structure and Function of GPCRs

GPCRs belong to the class of integral plasma membrane proteins and share a common receptor protein topology throughout the entire family. The structure paradigm is a seven helix bundle that spans the cell membrane in an almost perpendicular orientation, thereby establishing a functional link between the exterior and the cytoplasm of the



**Fig. (1).** Side-by-side stereo presentation of the  $\text{C}\alpha$  trace model of rhodopsin derived from various biophysical and bioinformatics studies. The helix bundle is shown in a sideview, the extracellular compartment being on the top. For details see references [22-31].

cell [6,18-20]. The seven transmembrane sequence stretches can be identified by hydrophobicity analyses since they exhibit an increased hydrophobic signature in a corresponding hydrophobicity profile. From numerous biophysical and biochemical studies it is now general accepted that GPCRs intercalate into the cell membrane with their *N*-terminus in the extracellular compartment, while the *C*-terminus reaches into the cytoplasm of the cell. The seven transmembrane helices (7TM domain) that constitute the central core domain of all GPCRs, are sequentially connected by extracellular and intracellular loops. Apart from variations in the primary structure, GPCRs differ in length of these loops, as well as in length and function of both *N*- and *C*-termini. The ACTH (adrenocorticotropic hormone) receptor is one of the smallest GPCRs known with 297 residues. Biogenic monoamine receptor sequences cover a size from approximately 350 to 600 residues, peptide receptor sequences are found between 400 and 750 residues, while the mGluRs (metabotropic glutamate receptor) mark the upper boundary consisting of roughly 1200 amino acid residues [21].

Even though no high-resolution structure of any pharmaceutical relevant member of the GPCR superfamily has been determined by e.g. x-ray crystallography, low resolution models derived from electron cryo-microscopy and electron diffraction of bovine, frog and squid rhodopsin reveal a detailed picture of the insertion mode of each helix within the context of the transmembrane helix bundle domain (Fig. (1)) [22-31].

From a functional point of view, GPCRs share a common property in that they work as transmembrane

transducer systems by transferring an extracellular message across the cell membrane, thus allowing the affected tissue to respond to a broad range of signalling molecules [32-35]. Upon extracellular binding of the molecular stimulus, the central core domain (7TM domain) is believed to undergo a conformational change, thereby transmitting the extracellular binding event into the cytoplasm (Fig. (2)). The binding of a receptor agonist leads to an intracellular interaction of the receptor protein with its cognate heterotrimeric GDP-bound G protein. The agonist-promoted conformational change of the receptor protein followed by the cytoplasmic G protein-coupling initiates the activation of intracellular effector systems by the G protein cycle (Fig. (2)). The coupling event catalyzes the exchange of GDP against GTP and the dissociation of the GTP-bound  $\alpha$  subunit from the  $\beta\gamma$  heterodimer. Depending on the very nature of the G protein  $\alpha$  subtype, different effector systems such as enzymes (e.g. adenylyl cyclase, phospholipase C) or ion channels are functionally modulated, which substantially amplifies the production of second messengers. The effector activation event is accompanied by a GTPase activity of the  $\alpha$  subunit releasing inorganic phosphate. The GDP-bound form converts the  $\alpha$  subunit to exhibit high affinity for the  $\beta\gamma$  heterodimer, finally forming the GDP-bound heterotrimeric G protein again. The modulated concentration of second messengers elicits phosphorylation cascades across the cytoplasm to the nucleus, eventually activating the final physiological response of a cell to the original extracellular stimulus. Even though this functional paradigm accounts for all known GPCRs, this obvious convergence after the ligand binding event is diversified by the selective activation of only distinct types of G proteins from which e.g. numerous different  $G_\alpha$  subunits are known (Fig. (2)) [32-35].

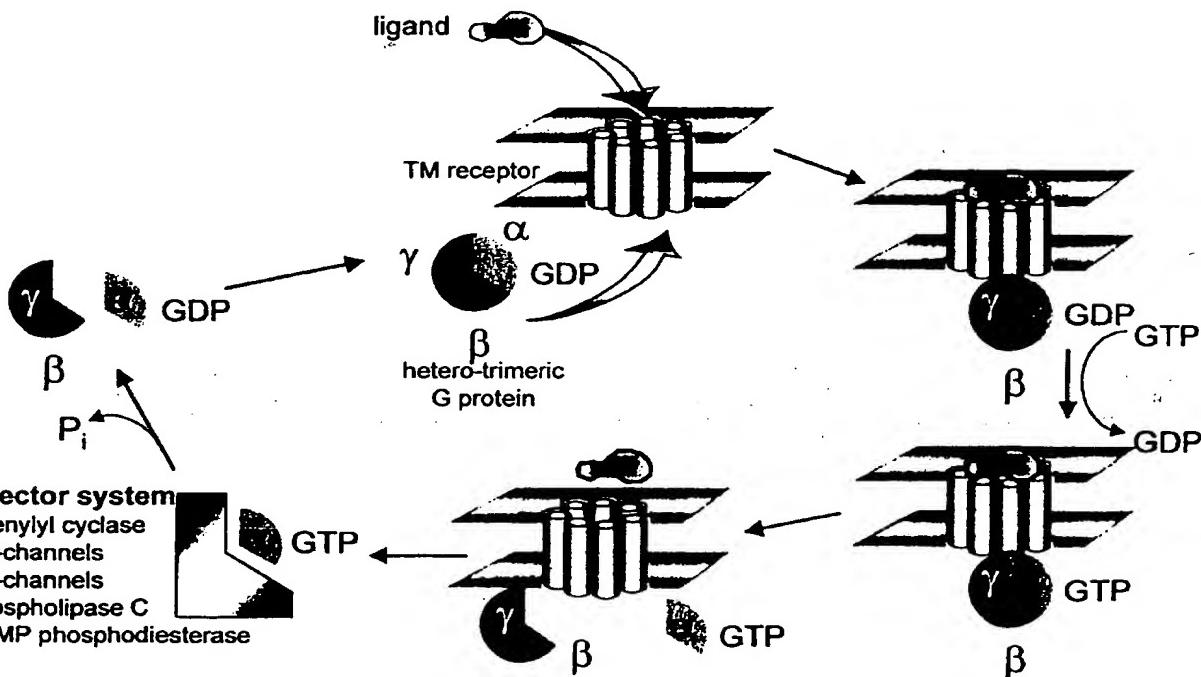


Fig. (2). Schematic representation of the ligand-GPCR interaction mediated G protein cycle.

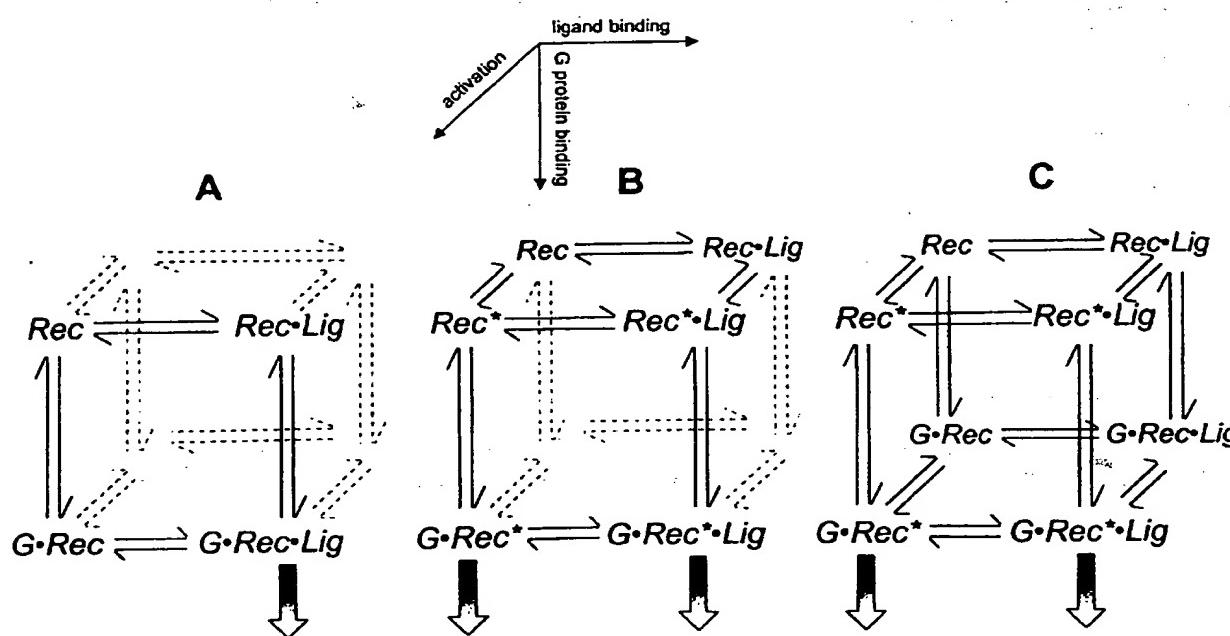
In order to fully characterize the mechanism of action of GPCRs, a thermodynamic "eight-state-model" has been developed as a mechanistic hypothesis describing the macroscopic properties of transitions among distinct conformational states (Fig. (3)) [36]. The simplest way to describe the ligand-induced receptor activation event is a ternary complex model (A) that defines two distinct affinity states of the receptor for agonist binding, notably the free receptor (*Rec*) and the G protein-bound form (*G*•*Rec*) (Fig. (3)A). Agonists would display high affinity to the G protein-associated receptor, while antagonists would exhibit only low-affinity towards the complex. With the discovery that GPCRs can activate G proteins in the absence of any agonist, the simple ternary complex model required an extension. To account for the existence of such constitutively active GPCRs, a receptor activation step in the unliganded form was introduced (Fig. (3)B). This receptor isomerization hypothesis resulted in a "six-state-model" in which the activated receptor (*Rec*<sup>\*</sup>) is capable of signalling in both the G protein-associated form (*G*•*Rec*<sup>\*</sup>), and in the ternary complex (*G*•*Rec*<sup>\*</sup>•*Lig*). The problem with that receptor activation-extended ternary complex model is that the G protein only binds to the receptor in its activated form *Rec*<sup>\*</sup>. Experimental evidence clearly suggests that G proteins do also bind to the resting state (*Rec*) without subsequent G protein activation. To account for these findings and to refer to the microscopic reversibility principle of thermodynamics, an "eight-state-model" was proposed in which the receptor protein can undergo three distinct processes, namely (i) ligand binding, (ii) receptor isomerization, and (iii) G protein binding (Fig. (3)C). Agonists can bind to four different receptor states clearly favouring the activated states

generated either by receptor isomerization or by G protein association. Inverse agonists would prefer to bind the non-activated groundstate (*Rec*), while partial agonists show affinity to both receptor states but still cause receptor activation. In the thermodynamic "eight-state-model" an antagonist would just block the interconversion of different states rather than preferably bind to distinct states (Fig. (3)) [36].

In order to address phenomena such as isosteric or allosteric antagonism, structural models with atomic resolution are mandatory that are actually frequently used for both rationalizing structure-activity relationships of low molecular weight agonists and antagonists, as well as understanding the results from site-directed mutagenesis experiments. A detailed discussion of the actual status of experimentally derived, and molecular modeling derived GPCR structures [37] is beyond the scope of this review, since this contribution is mainly aimed to introduce the currently applied technologies to identify compounds selectively modulating peptide-binding GPCRs.

### GPCR Classification

Exhaustive sequence analysis revealed three major homology families for the mammalian GPCRs, notably the family 1 or rho-family (prototype: rhodopsin), the family 2 or scr-family (prototype: secretin receptor), and the family 3 or mGluR family (prototype: metabotropic glutamate receptors) receptors (Fig. (4)) [32-35]. Family 1 receptors are divided into further subfamilies according to the size and



**Fig (3).** Mechanistic characterization of GPCR activation; A: "four-state" model; B: "six-state" model; C: "eight-state" model. Rec: receptor protein; Rec<sup>\*</sup>: activated receptor protein; G: G protein; Lig: ligand molecule; filled arrows mark complexes capable of signalling (for details see text).

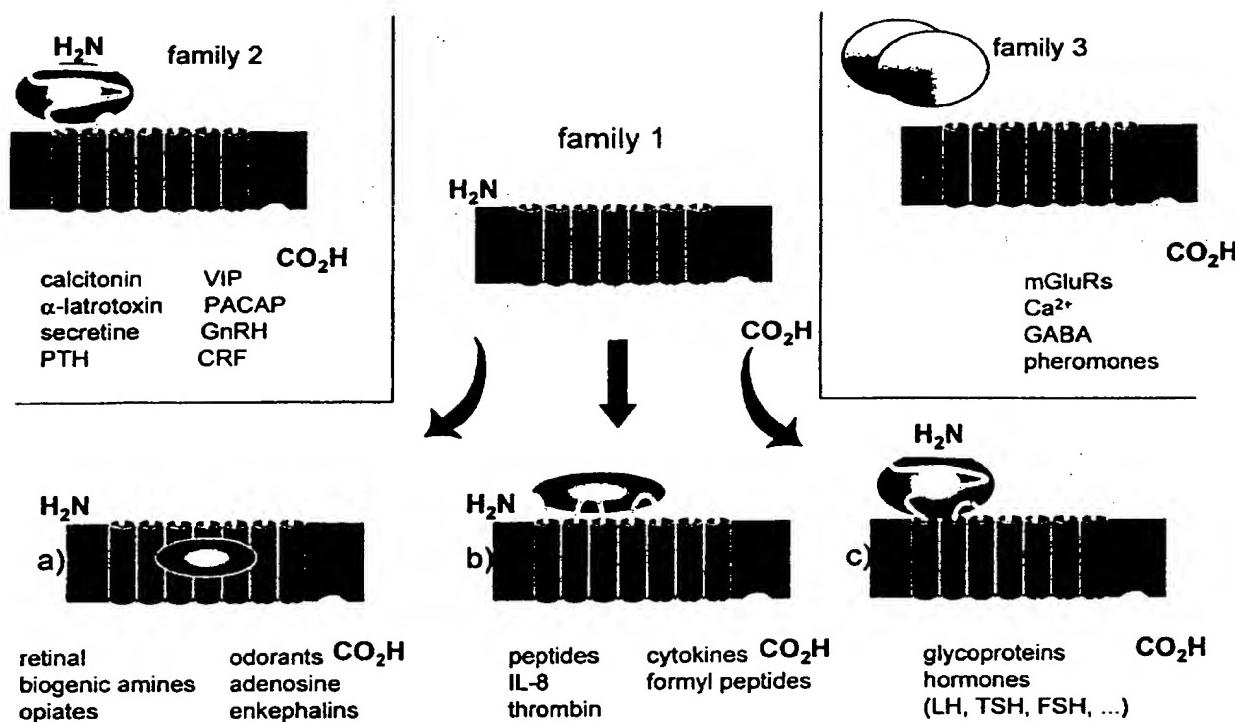


Fig. (4). Sequence homology-derived classification of GPCRs. Each GPCR family is characterized by a common ligand binding mode.

chemical nature of their corresponding agonists, as well as the mode of ligand binding. Family 1a accommodates the  $\beta$ -adrenoceptor-type receptors that are activated by small ligands such as biogenic monoamines, opiates, nucleotides, and small peptides, that comparably bind to a transmembrane cavity formed by helices 3, 4, 5, and 6. Family 1b is composed of receptors stimulated by oligopeptides and proteins such as IL-8 (interleukin-8), cytokines, and thrombin. The ligand binding epitope is located in the extracellular loop region. Family 1c receptors recognize glycoprotein hormones such as LH (luteinizing hormone), TSH (thyroid-stimulating hormone), and FSH (follicle-stimulating hormone) while their ligand binding site is centred in a large extracellular N-terminal domain (Fig. (4)).

Family 2 receptors are distinct from rho-family receptors in that they bind large peptides like glucagon, secretin, PTH (parathyroid hormone), VIP (vasointestinal peptide), or CRF (corticotropin-releasing factor). Comparable to family 1c receptors, the secretin family utilizes a large N-terminal domain for ligand binding. Family 3 receptors are unique since they possess a large extracellular N-terminal domain of several hundred residues that constitutes the binding site for smallish ligands such as a single divalent  $\text{Ca}^{2+}$  cation, glutamate, GABA ( $\gamma$ -amino butyric acid), and pheromones (Fig. (4)).

On the light of this classification, peptide-binding receptors are not structurally homogenous since they belong to family 1 and 2. Consequently, correlation of sequence homology with ligand similarity remains questionable which is also reflected by the mutual different binding modes of peptidic and non-peptidic agonists and antagonists.

#### Ligand Variety

GPCRs are stimulated by an amazingly large number of agonists covering a broad range of chemical diversity. Ligands are as small as divalent cations, biogenic monoamines such as acetylcholine or serotonin, fragrances and taste molecules such as aspartame or limonene, single amino acids such as glutamate or GABA, or nucleotide analogues such as adenosine. Medium-sized ligands range from cannabinoids over prostaglandines to small oligopeptides such as enkephalins, angiotensin II, bradykinin, somatostatin, and tachykinins. Larger oligopeptides and globular proteins constitute the family of macromolecular ligands including e.g. neuropeptide Y, C5a anaphylatoxin, interleukin-8, or chemokines. Even proteolytic enzymes such as thrombin, which activates its receptor by cleaving off an N-terminal peptide, selectively bind to distinct members of the GPCR superfamily. Apart from their important role in sensory perception including

vision, smell, and taste, GPCRs are obviously optimized by Nature for recognition and transduction of messages from different compound classes, i.e. nucleosides, lipid mediators, neurotransmitter, peptides, and proteins [6,18,38].

In this context, it is interesting to note that the majority of GPCR-targeted therapeutic principles exploit only a single compound class, notably the neurotransmitters. When the number of currently identified neurotransmitter receptors is compared with the number of disease-relevant peptide-binding GPCRs, an obvious imbalance becomes apparent in that only a small number of peptide-binding GPCRs is targeted by established therapies. Agonism and antagonism of e.g.  $\alpha$  and  $\beta$  adrenoceptors, dopamine, histamine, serotonin, or muscarinic acetylcholine receptors are well established therapeutic principles for numerous "best-selling" drugs covering virtually all therapeutic areas, including gastrointestinal, cardiovascular, and CNS indications. In contrast, only two peptide-binding GPCR families are addressed by marketed non-peptide drugs, namely the opioid receptors and the angiotensin II receptor. However, the importance of peptide- and protein-binding GPCRs for drug discovery continues to be manifested by the fact that across

current pharmaceutical research, especially in industry, numerous projects are pursued to identify leads that, upon optimizations fulfil all pharmacodynamic and pharmacokinetic demands required for clinical applicability (Table 1).

## CLASSICAL LEAD FINDING AND DRUG DEVELOPMENT

Currently applied drug design and discovery approaches are typically classified as rational or random, depending on whether or not structural rationales are employed. The area of GPCR agonists and antagonists research is mainly driven by screening approaches in which large numbers of randomly selected chemical entities are tested in high-throughput screens. These shotgun procedures provide a practical means for identifying new leads for a particular receptor. In the following, this classical approach for GPCR-targeted drug discovery will be exemplified with prototype studies conducted on the angiotensin II, endothelin, bradykinin, neurokinin, and NPY receptors, respectively.

**Table 1. Selection of endogenous Peptides that Exert their Biological Activity by Selective Activation of a GPCR**

GPCR	code	native ligand (peptide/protein)	nature of the ligand
angiotensin receptors	AT <sub>1</sub> , AT <sub>2</sub>	angiotensin II (All)	Asp-Arg-Val-Tyr-Ile-His-Pro-Phe
bombesin receptors	BB1 - BB4	bombesin, neuromedin B, gastrin-releasing peptide	14 aa peptide amide
bradykinin receptors	B <sub>1</sub> , B <sub>2</sub>	bradykinin (BK)	Arg-Pro-Pro-Gly-Phe-Ser-Pro-Phe-Arg
C3a receptor	C3aR	C3a anaphylatoxin	protein
C5a receptor	C5aR	C5a anaphylatoxin	protein
CC chemokine receptors	CCR1 - CCR9	chemokines	proteins
CXC chemokine receptors	CXCR1 - CXCR5	chemokines	proteins
cholecystokinin/gastrin receptors	CCK <sub>A</sub> , CCK <sub>B</sub>	cholecystokinin (CCK), gastrin	33 aa peptide amide, 17 aa peptide amide
endothelin receptors	ET <sub>A</sub> , ET <sub>B</sub>	endothelin-1 (ET-1), ET-2, ET-3	21 aa peptides
alpha factor pheromone receptor	STE2, STE3	fungal mating pheromones	13 aa peptide
fMet-Leu-Phe receptor	fMLP-R	Formylpeptide (fMLP)	fMet-Leu-Phe
galanin	GAL1, gal2, gal3	galanin	30 aa peptide
melanocortin receptors & ACTH receptor	MC <sub>1</sub> , MC <sub>2</sub> , MC <sub>4</sub> , MC <sub>5</sub> MC <sub>2</sub> = ACTH receptor	melanocortin (MSH) adrenocorticotrophic hormone (ACTH), corticotropin	39 aa peptide
neuropeptide Y receptor	Y <sub>1</sub> - Y <sub>6</sub>	neuropeptide Y (NPY), peptide YY (PYY), pancreatic polypeptide (PP)	36 aa peptide amide (NPY)
neurotensin receptor	NTS1, nts2	neurotensin	13 aa peptide
opioid receptors	$\delta$ $\kappa$ $\mu$	[Met]-enkephalin, [Leu]-enkephalin dynorphin A $\beta$ -endorphin, Lipotropin C fragment	Tyr-Gly-Gly-Phe-Met/Leu 17 aa peptide 31 aa peptide
nociceptin receptor	ORL1	nociceptin, orphanin FQ	17 aa peptide
somatostatin receptors	sst <sub>1</sub> - sst <sub>5</sub>	somatostatin	cyclic 14 aa peptide
tachykinin receptors	NK <sub>1</sub> NK <sub>2</sub> NK <sub>3</sub>	substance P neurokinin A (NKA), substance K, neuromedin L neurokinin B (NKB), neuromedin K	11 aa peptide His-Lys-Thr-Asp-Ser-Phe-Val-Gly-Leu-Met-NH <sub>2</sub> Asp-Met-His-Asp-Phe-Phe-Val-Gly-Leu-Met-NH <sub>2</sub>
thrombin / protease-activated receptors	PAR1, PAR2, PAR3, PAR4	thrombin, trypsin, factor Xa	protein

(Table 1). contd....

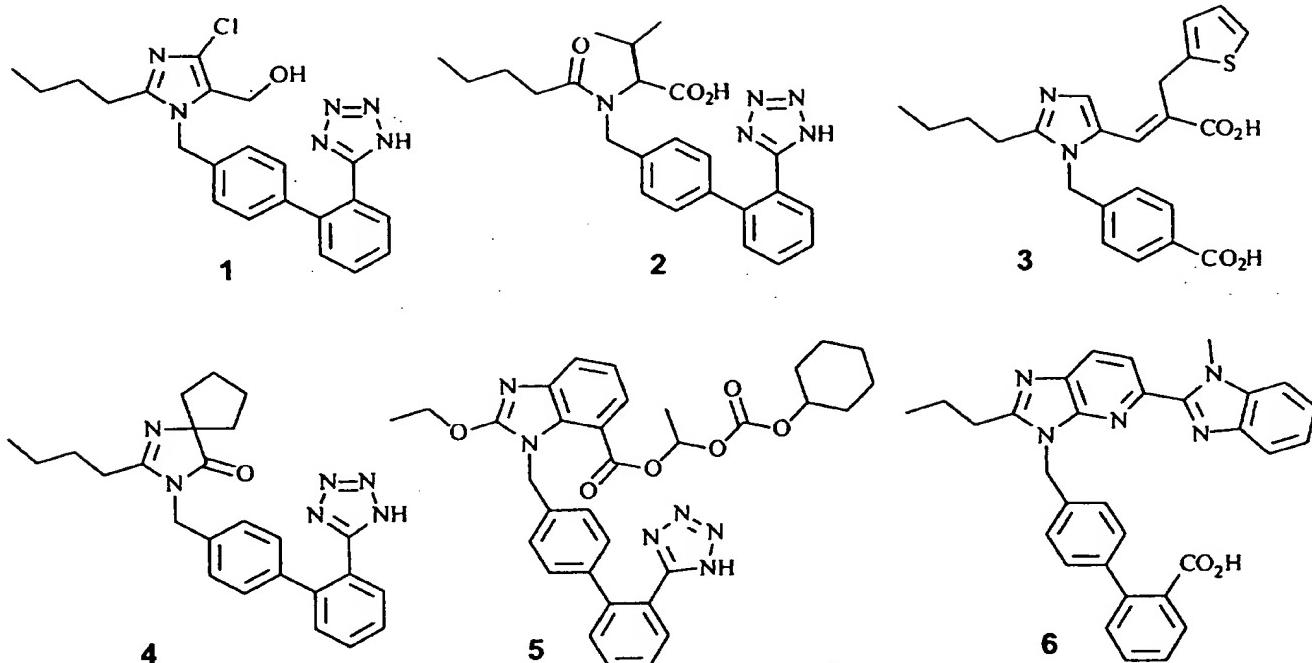
GPCR	code	native ligand (peptide/protein)	nature of the ligand
vasopressin receptors	V1A, V1B, V2	vasopressin	Cys-Tyr-Phe-Gln-Asn-Cys-Pro-Arg-Gly-NH <sub>2</sub>
oxytocin receptor	OT	oxytocin	Cys-Tyr-Ile-Gln-Asn-Cys-Pro-Leu-Gly-NH <sub>2</sub>
vasotocin receptor	VT	vasotocin	Cys-Tyr-Ile-Gln-Asn-Cys-Pro-Arg-Gly-NH <sub>2</sub>
orexin receptors	OX <sub>1</sub> , OX <sub>2</sub>	orexin A/B	33 aa/28 aa peptide amides
FSH receptor	FSH receptor	follicle-stimulating hormone (FSH)	protein
LSH receptor	LSH receptor	luteinizing, choriogonadotrophic hormone, luteinizing hormone	protein
TSH receptor	TSH receptor	thyrotropin, thyroid-stimulating hormone	protein
LHRH receptor	LHRH receptor	gonadotropin-releasing hormone (GnRH), luteinizing hormone-releasing hormone (LHRH)	pGlu-His-Trp-Ser-Tyr-Gly-Leu-Arg-Pro-Gly-NH <sub>2</sub>
thyrotropin-releasing hormone & secretagogue receptors	TRH <sub>1</sub> , trh <sub>2</sub>	thyrotropin-releasing hormone/factor (TRH/F)	pGlu-His-Pro-NH <sub>2</sub>
GHS receptor	GHSR1a, GHSR1b	growth hormone secretagogues (GHS)	oligopeptides
calcitonin/calcitonin gene-related peptide receptors	CGRPR	calcitonin, calcitonin gene-related peptide (CGRP)	32 aa peptide amide
amylin receptor	amylin receptor	amylin	37 aa peptide amide
adrenomedullin receptor	adrenomedullin receptor	adrenomedullin	52 aa peptide amide
corticotropin-releasing factor receptor	CRF <sub>1</sub> , CRF <sub>2</sub>	corticotropin-releasing factor (CRF)	41 aa peptide amide
gastric inhibitory peptide receptor	gip receptor	gastric inhibitory peptide (GIP)	42 aa peptide
glucagon/glucagon-like peptide receptor	GLP1	glucagon	29 aa peptide
growth hormone-releasing hormone receptor	GHRH receptor	growth hormone-releasing hormone/factor (GHRH/GRF)	44 aa peptide amide
parathyroid hormone receptor	type 1, type 2	parathyroid hormone (PTH)	84 aa peptide
secretin receptor	secretin receptor	secretin	27 aa peptide amide
vasoactive intestinal peptide & PACAP receptor	VPAC <sub>1</sub> , VPAC <sub>2</sub> , PAC <sub>1</sub>	vasoactive intestinal peptide (VIP) pituitary adenylate cyclase activating peptide (PACAP)	28 aa peptide amide 38 aa peptide

### Angiotensin-II Antagonists

#### Biomedical Significance

The endogenous octapeptide hormone angiotensin-II (A-II) (Table 1), Asp-Arg-Val-Tyr-Ile-His-Pro-Phe, is the key effector compound of the renin-angiotensin system (RAS) which is one of the main blood pressure and electrolyte/fluid homeostasis regulating system in mammals [39]. As a result of a proteolytic cascade starting with angiotensinogen, angiotensin-II is released from its precursor decapeptide angiotensin-I by the action of angiotensin-I converting enzyme (ACE), the latter being a qualified target of antihypertensive drugs [40]. The conversion from angiotensinogen to angiotensin I is catalyzed by the aspartic protease renin, peptide-type inhibitors of which have not yet reached an advanced state of clinical development [41]. A-II interacts specifically with two different receptor subtypes of

the GPCR superfamily, notably the AT<sub>1</sub> and the AT<sub>2</sub> receptor, respectively [21]. Interaction with the AT<sub>1</sub> receptor causes severe vasoconstriction, aldosterone release, vasopressin secretion, and renal sodium reabsorption. These effects convergently result in a dramatic increase of extracellular fluid volume, thus giving rise for a significant hypertensive effect. Therapeutic intervention into the RAS clearly offers major clinical and commercial success as shown with the ACE inhibitors for the treatment of hypertension and congestive heart failure [40]. Due to the fact that ACE inhibitors cause dry cough and angioedema [42], new strategies have been sought to block the vasoconstrictory activities of the biologically active player, A-II [43]. Specific inhibition of the A-II target receptor interaction, the final step of the RAS, offers an entirely new and selective approach to blocking this regulatory system regardless of the source of the biological active peptide. And indeed, selective nonpeptide A-II antagonists emerged as a new class of



**Fig. (5).** Structures of marketed A-II antagonists.

antihypertensives on the cardiovascular drug market exemplified by the released drugs Losartan 1 [44,45], Valsartan 2 [46], Eprosartan 3 [47], Irbesartan 4 [48], Candesartan 5 [49], and Telmisartan 6 [50], respectively (Fig. (5)).

Consequently, the angiotensin receptor represents one of the most advanced drug targets from the family of peptide-binding (non-opioid) GPCRs in the sense that screening hits have successfully been transferred to leads, further to development candidates that finally reached the drug market as safe and innovative drugs introducing a new therapeutic principle.

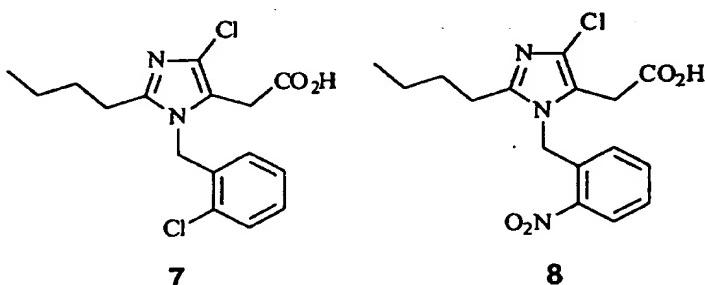
#### Lead Finding

In the search for A-II antagonists potent peptides have been synthesized in a classical ligand-based design concept, yielding e.g. [Sar<sup>1</sup>,Ala<sup>8</sup>]-Angiotensin-II, commonly termed Saralasin [51]. However, all these peptides display limited therapeutic value as potential antihypertensives due to their poor oral bioavailability, rapid excretion, structural complexity, and significant agonistic profiles [51,52].

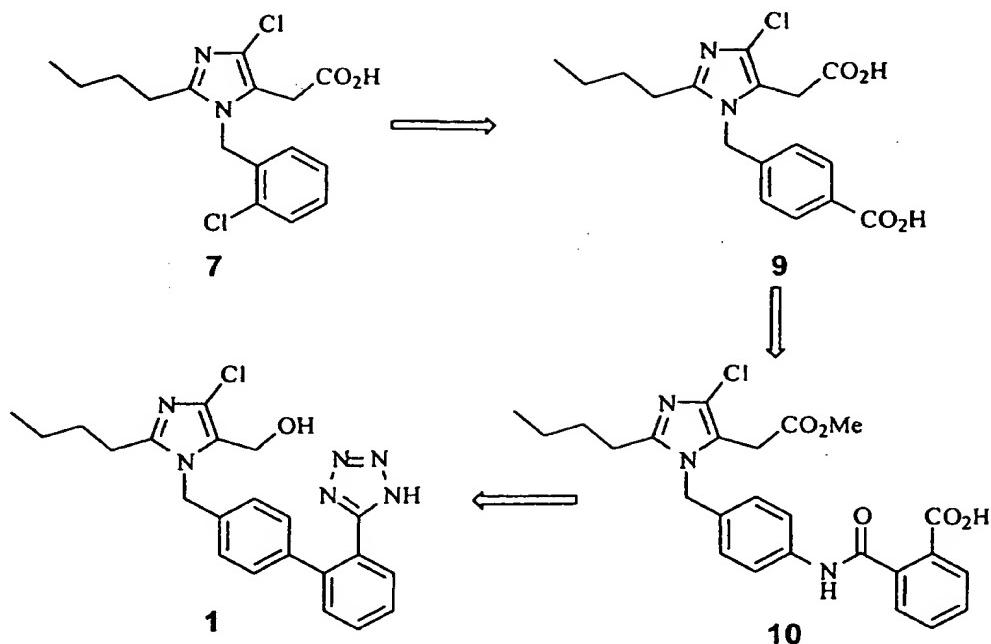
The feasibility of identifying nonpeptide A-II receptor binding compounds with purely antagonistic profile was demonstrated by a research group at Takeda Chemical Industries in 1982. In a series of two patents, Furukawa and co-workers reported on the inhibition of angiotensin-II-induced contractile response in rabbit aorta by numerous different 1-benzylimidazole-5-acetic acid derivatives (Fig. (6)) [53]. The two compounds S-8307 7 and S-8308 8 mark the beginning of a new era of antihypertensive drug research in which almost any pharmaceutical company attempted to derive new compounds from that initial findings.

#### Drug Development

The Takeda compounds served as lead structures for the development of highly potent and selective analogues at DuPont that culminated in Losartan 1 (DuP-753, EXP-7711), the first nonpeptide A-II antagonist that got approval by the FDA and reached the market (Fig. (7)). Guided by molecular modeling studies, the substitution pattern of the benzylic phenyl-ring was changed yielding EXP-6155, 9 which displayed a ten-fold increased binding affinity over e.g. S-8307 7 [54]. Further extension in *para*-position of the



**Fig. (6).** Initial lead structures disclosed by Takeda Chemical Industries.

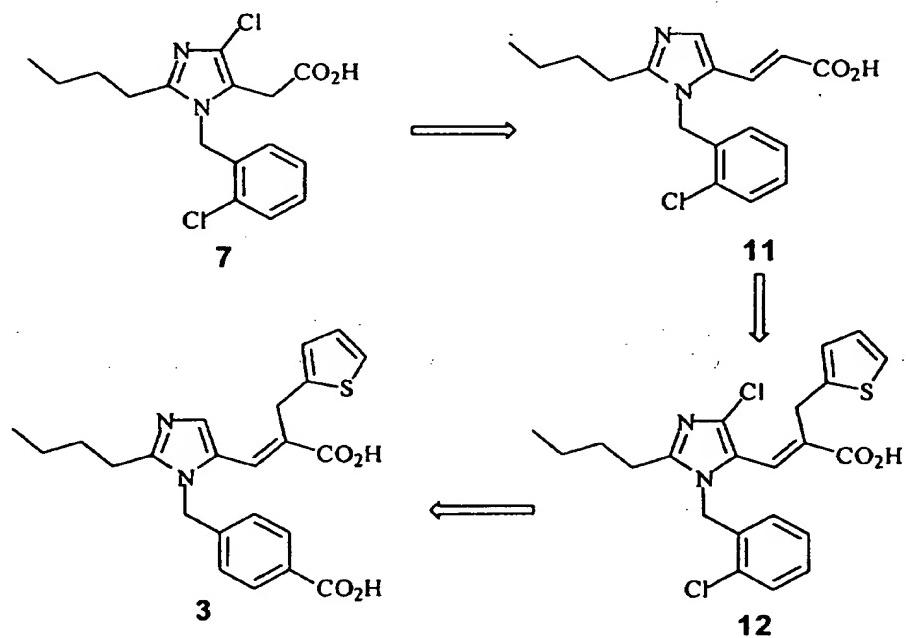
**Fig. (7).** Development of Losartan 1.

aromatic ring resulted in more potent analogues as shown with EXP-6803 10 [55].

The deletion of the interaromatic carboxamide linkage yielding biphenylmethyl-substituted imidazole-5-acetic acid derivatives produced orally active compounds and subsequent exchange of the *ortho*-carboxylic acid on the terminal aromatic ring against the tetrazole moiety further improved the oral activity [56,57]. The imidazole-5-acetic acid substituent was modified to the corresponding alcohol

in the analogue chosen as clinical candidate. However, later it could be shown that the parent acetic acid sidechain of the imidazole core is the active metabolite of Losartan 1 [58].

Instead of modifying the N-1 substituent of the Takeda imidazole derivatives, 7 and 8, SmithKline Beecham decided to explore the 5 position in more detail (Fig. (8)). Introduction of an acrylic acid in that position (11) resulted in a 15-fold enhancement in binding affinity. Further introduction of a 2-thienylmethyl group in  $\alpha$ -position of the

**Fig. (8).** Development of Eprosartan 3.

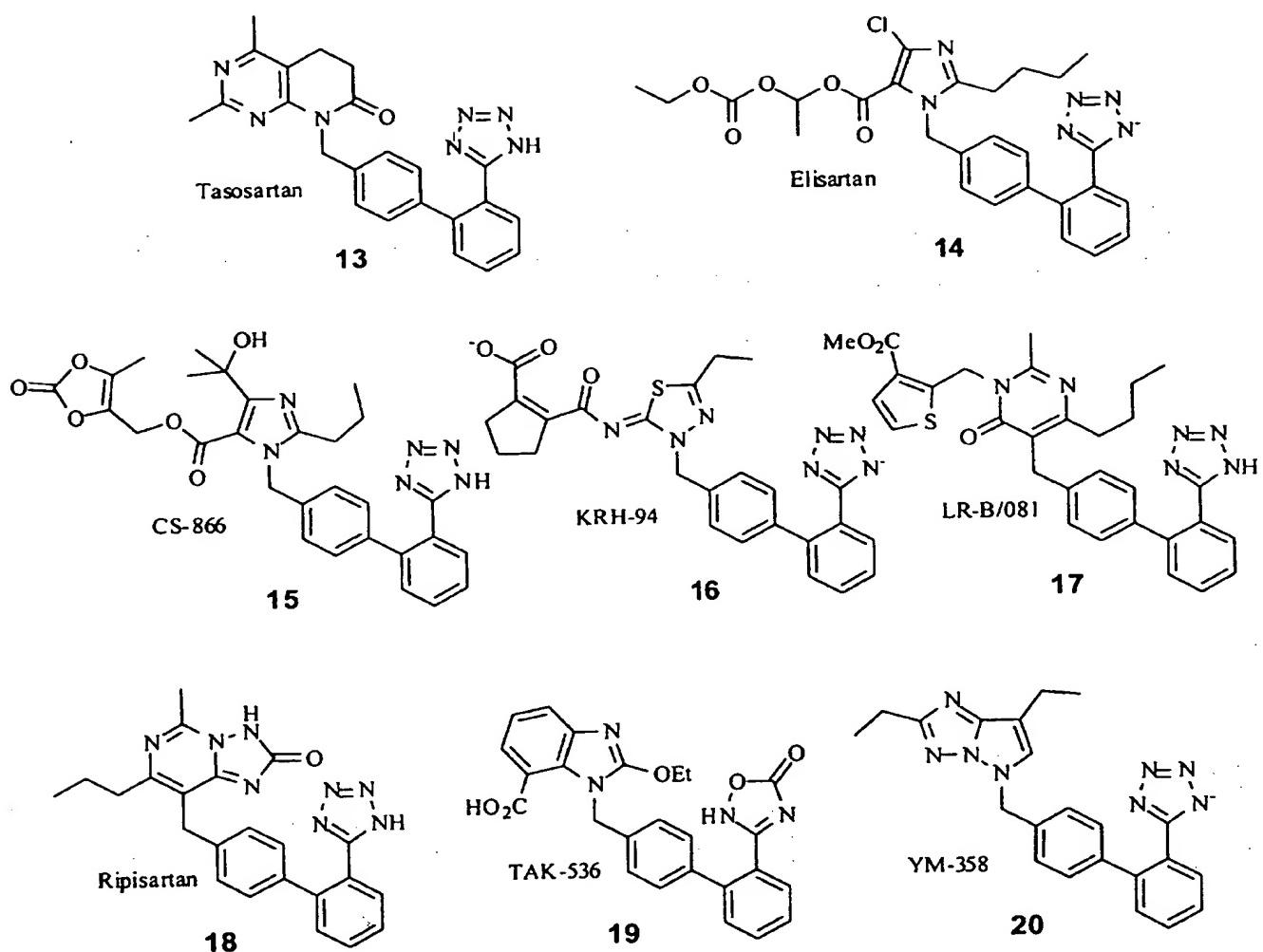


Fig. (9). Next-generation "sartans" in advanced states of clinical development.

acrylic acid substituent (12) together with a modification in the N-1 benzylic substituent finally yielded SK&F-108566, 3 [59,60] which inhibits A-II binding to its receptor in the single digit nanomolar range [61].

The Ciba compound CGP-48933, 2 (Fig. (5)) is the result of an optimization process attempting to replace the imidazole ring structure originally described by Takeda [53]. The 1-benzyl-2-butyl-4-chloro-imidazole-5-acetic acid is replaced with an N-terminally acylated amino acid, notably valine. CGP-48933, 2 has passed the clinical development and reached the market as Valsartan [62]. It is clearly beyond the scope of this review to systematically summarize the lead optimization programs pursued by the different pharmaceutical companies, however, it should be emphasized that, apart from the currently marketed drugs, numerous next-generation compounds and follow-ups in late clinical development are expected to get approved in the near future (Fig. (9)) [63,64]. These new "sartans" (13 - 20) together with the first generation drugs (1 - 6) will further change the landscape of antihypertensive prescription drugs since they clearly introduced a new quality of

antihypertensive principles into therapy of cardiovascular diseases.

Apart from these biomedical aspects, the development of the "sartans" acting specifically on a member of the GPCR superfamily evolved to a textbook example of protein-targeted drug design within modern medicinal chemistry [65].

### Endothelin

#### Biomedical Significance

Endothelin 1 (ET-1) is a 21 amino acid bicyclic peptide (Table 1) that was initially isolated from porcine aortic endothelial cells [66]. The endothelins constitute a class of three related isopeptides (ET-1, ET-2, ET-3) [67], exhibiting vasoconstrictive and mitogenic potential [68] upon binding to two receptor subtypes, notably the  $\text{ET}_A$  and  $\text{ET}_B$  receptor [69,70]. ET-1 selectively binds to the  $\text{ET}_A$  receptor which is expressed on vascular smooth muscle cells

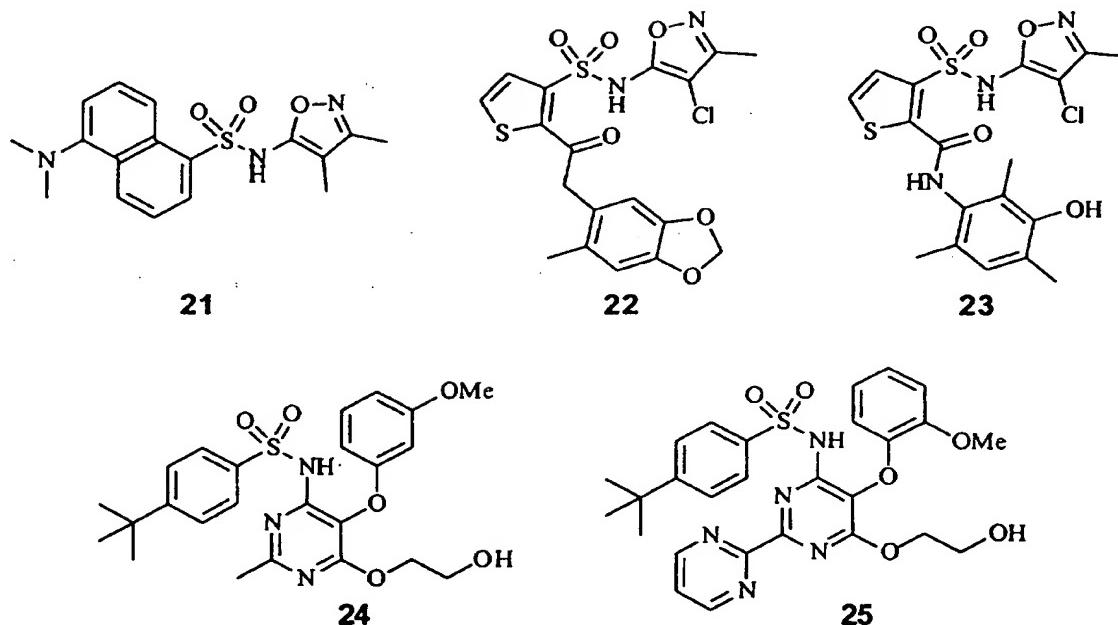


Fig. (10). Aryl-sulfonamide-type ET antagonists.

(lung, aortic, heart) and mediates vasoconstriction and proliferation through activation of a complex intracellular signalling cascade [71,72]. The  $\text{ET}_B$  receptor, localized in the brain, on vascular endothelial cells, and smooth muscle cells, is responsible for vasodilation via the release of nitric oxide, prostacyclin, and adrenomedullin [73,74]. In addition,  $\text{ET}_B$  functions as a clearance receptor for endogenous ET by the internalization of the receptor-ligand complex. On the other hand,  $\text{ET}_B$  may also cause vasoconstriction in some tissues [75].  $\text{ET}_A$  and  $\text{ET}_B$  receptors share high sequence similarity (app. 68%).  $\text{ET}-1$  is predominantly produced by endothelial cells acting in an autocrine and paracrine fashion as a mediator of vascular function. Elevated ET levels has been observed in tissue and plasma in a number of cardiovascular disorders, thereby contributing to disease states including hypertension [76], vasospasm, atherosclerosis [77], acute myocardial infarction [78], congestive heart failure [79,80], restenosis [81], subarachnoid hemorrhage, ischemia, pulmonary hypertension [82], and renal failure [83]. Due to the pivotal pathophysiological role of the endothelin receptor-ligand interaction, this receptor system emerged as a promising target for therapeutic intervention in the disease states mentioned above [84].

### Lead Finding

Since the discovery of  $\text{ET}-1$  in 1988, a large number of potent antagonists have been described [84]. The first antagonists emerging from random screening efforts have been reported in 1992. These first generation compounds comprise anthraquinones from *Streptomyces misakiensis*, steroids isolated from bayberry, *Myrica cerifera*, and diphenyl ethers discovered in fungal broths [85]. Lead finding in this field is mainly based on compound library

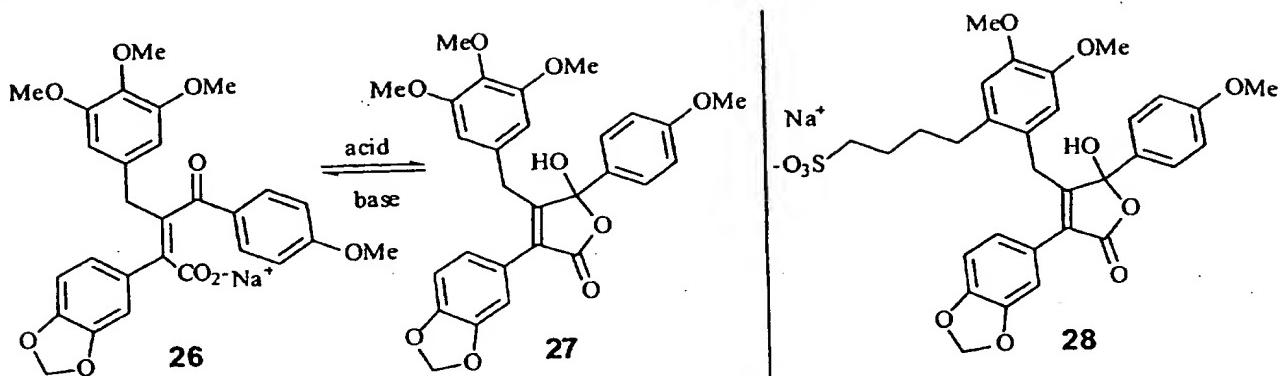
screening followed by classical lead optimization within medicinal chemistry programs. A number of peptide-based antagonists have been reported including the prominent cyclic pentapeptide BQ-123, and other peptide antagonists, e.g. BQ-788, FR-139317, PD145065, PD156252, RES-701-1, TAK-044, and IRL2500 [84-88].

As mentioned above, this review, will focus on the development of nonpeptide antagonists emerging from those programs directed towards the discovery of active low molecular weight compounds. Primarily, the  $\text{ET}_A$ -selective antagonists as well as antagonists exposing mixed  $\text{ET}_A/\text{ET}_B$  affinity play a major role for therapeutic intervention, even though some  $\text{ET}_B$ -selective antagonists have been reported only recently.

### Aryl Sulfonamides

Bristol Myers Squibb designed BMS182874, 21, a nonpeptide  $\text{ET}_A$ -selective antagonist from an initial hit which was discovered by screening of a sulfathiazole library [89]. The sulfonamide BMS182874, 21, exhibits an  $\text{IC}_{50}$  value of 150 nM at the  $\text{ET}_A$  receptor (A10 cells) and shows no binding affinity to the  $\text{ET}_B$  receptor (Fig. (10)).

From a similar series of compounds, Immunopharmaceuticals (Texas Biotech.) developed an isoxaolyl-thiophene sulfonamide, TBC-11251, 22 (Sifaxsentan) [90]. This orally active compound has shown efficacy in phase II clinical trial of congestive heart failure (CHF) and demonstrated activity in a rat model of myocardial infarction and acute hypoxia-induced pulmonary hypertension (PH) [91]. Further investigations established a unique pharmacophore framework, characterized by a central thiophene subunit for selective  $\text{ET}_A$  antagonism [92]. Maintaining the sulfonamide substituent in position 3 and altering the substituent in position 2 in the thiophene ring



**Fig. (11).** Butenolide-type ET antagonists.

led to a series of compounds with enhanced pharmacological properties. TBC-2576, 23, the optimal analogue in this series showed about 10-fold higher  $ET_A$  binding affinity compared to Sitaxsentan, 22, and high  $ET_A$ -selectivity, as well as a serum half-life of 7.3 h in rats, paired with *in vivo* activity (Fig. (10)) [92].

A number of nonpeptide ET<sub>A</sub>/ET<sub>B</sub> antagonists based on a pyrimidyl-benzene sulfonamide scaffold have been reported. The first example for an orally active representative is Ro46-2005, 24 [93] which was obtained after optimization of a lead compounds identified by random screening in an antidiabetic project. The binding affinities of Ro46-2005, 24 ( $K_i=220$  nM (ET<sub>A</sub>),  $K_i=1000$  nM (ET<sub>B</sub>)) could further be optimized yielding the bipyrimidyl-benzene analogue Ro47-0203, 25 (Bosentan) which represents an improvement in both, receptor binding affinities ( $K_i=4.7$  nM (ET<sub>A</sub>),  $K_i=95$  nM (ET<sub>B</sub>)) and oral activity (Fig. (10)) [94]. Bosentan 25 is a competitive mixed ET<sub>A</sub>/ET<sub>B</sub> antagonist and shows promising results in clinical trials [88] in terms of vasodilation. Further, it improves left ventricular performance and reduces renal dysfunction. The beneficial effects of Bosentan 25 have been characterized in CHF models, in hypertension related experiments and in subarachnoid hemorrhage (SAH) trials. These and other potential applications have been described in a recent review by Roux *et al.* [88].

## Butenolides

CI-1020, also known as PD156707, 26, 27 [95] emerged from the optimization of an initial lead structure which was identified from library screening (Fig. (11)). The optimization procedure was guided by following the *Topliss* "decision tree" approach based on QSAR principles [96]. CI-1020, 26, 27 represents the first clinical candidate emerging from the Parke-Davis series of butenolides. With an IC<sub>50</sub> value of 0.30 nM on recombinant human ET<sub>A</sub> receptor (IC<sub>50</sub>=780 nM (ET<sub>B</sub>)) it demonstrates high ET<sub>A</sub>-selectivity (2600-fold). CI-1020, 26, 27 undergoes tautomerization, thereby establishing the  $\gamma$ -hydroxy butenolide structure 27 under acidic conditions, while at basic pH the equilibrium is shifted in favour of the ring-opened  $\gamma$ -keto acid salt structure 26 [95]. The poor water-solubility of this compound, caused by cyclization, has driven the drug development process towards a series of water-soluble ring-closed  $\gamma$ -hydroxy

butenolides applicable for parenteral use [97]. One of the follow-up compounds exhibits promising pharmacological profiles by displaying improved activity compared to CI-1020, 26, 27 e.g. in preventing acute hypoxia-induced pulmonary hypertension (PH) in rats.

Most promising characteristics were found for an analogue containing the sodium salt of a sulfonic acid in compound 28 (Fig. (11)) [97]. It shows high ET<sub>A</sub>-selectivity (4200-fold) with an IC<sub>50</sub> value of 0.38 nM (ET<sub>A</sub>) and ET<sub>A</sub> functional activity of K<sub>B</sub>=7.8, which is similar or even superior to the progenitor CI-1020 26, 27. Moreover, it displays improved water-solubility and shows higher activity after i.v. infusion in preventing acute hypoxia-induced PH in rats (ED<sub>50</sub>=0.3 µg/kg/h) when compared to CI-1020 26, 27 [97]. The new compounds are currently evaluated in preclinical trials, while CI-1020 26, 27 has already been tested in a model of acute stroke and has entered clinical development for cerebral ischemia.

## Indane Carboxylic Acids

SB209670 29 emerged from the SmithKline Beecham laboratories after optimization of an initial hit discovered from compound library screening (Fig. (12)) [98]. Within a molecular modeling-driven approach based on a comparison of the NMR-derived conformation of ET-1 with the primary hit, an indene carboxylic acid derivative, the mixed ET<sub>A</sub>/ET<sub>B</sub> receptor antagonist SB209670 29 was designed ( $K_i=0.43$  nM (*hET<sub>A</sub>*)),  $K_i=14.7$  nM (*hET<sub>B</sub>*)). When administered *i.v.* SB209670 29 shows efficacy in different animal models of ET-mediated disease states, e.g. renal failure, hypertension [84], and ischemia-induced stroke. Due to the low oral bioavailability (4%) a structurally related analogue, SB217242 30 [99] was investigated that displays improved pharmacokinetics and bioavailability [86]. SB209670 29 is under development (phase I) for acute *i.v.* indications with efficacy in pulmonary hypertension (PH), chronic renal failure (CRF) and stroke [87], while SB217242 30 (phase I) is in development for chronic PH and chronic obstructive pulmonary disease (COPD) [87,100].

## Pyrrolidine Carboxylic Acids

The SmithKline Beecham compound SB209670 29 (Fig. (12)) served as template for the design of the

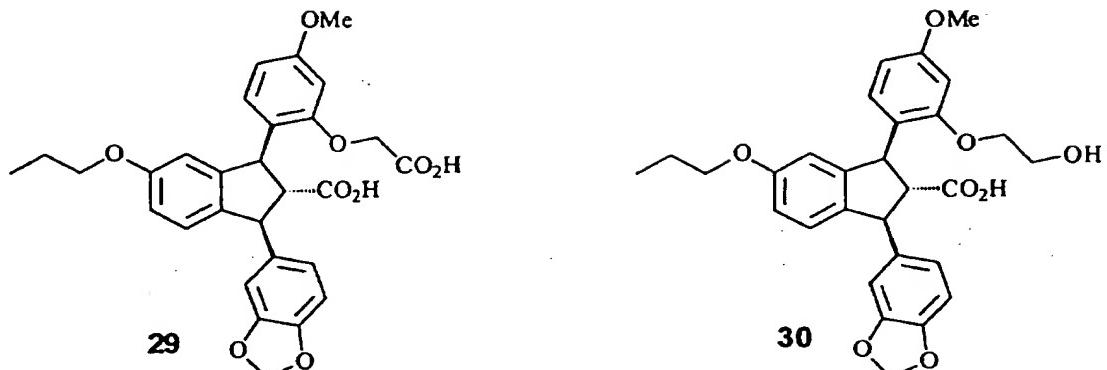


Fig. (12). Indane carboxylic acid-type ET antagonists.

pyrrolidine carboxylic acid A-127722 *rac*-31 (Fig. (13)) [101], that has been disclosed as a potent, ET<sub>A</sub>-selective antagonist, currently tested in clinical trials (PH, CHF) [87]. A-127722 *rac*-31 was reported to prevent dose-dependently cerebral edema in stroke-prone spontaneously hypertensive rats [100]. ABT-627 31, the active enantiomer (*2R,3R,4S*) of the *trans-trans* configurated 2,3,4-trisubstituted pyrrolidine ring, shows an IC<sub>50</sub> value of 0.08 nM on ET<sub>A</sub> and 8.1 nM on ET<sub>B</sub> [102]. The 1800-fold selectivity was dramatically altered by subtle structural modifications of A-127722 *rac*-31, which led to A-182026 32 with an ET<sub>A</sub>/ET<sub>B</sub> selectivity ratio of 3, thus being the most potent balanced dual

ET<sub>A</sub>/ET<sub>B</sub> antagonist known today. Replacement of the dialkyl-acetamide (*rac*-31) against a 2,6-dialkyl-acetanilide resulted in an ET<sub>B</sub>-selective antagonist, A-192621 33 exhibiting promising pharmacological properties [103]. Combination of the structure-activity relationships (SAR) derived from the first series of ET<sub>A</sub>-selective compounds (e.g. ABT-627 31) and the second series of ET<sub>B</sub>-selective antagonists (e.g. A-192621 33) led to a further optimized series of compounds. Therein A-308165 34 has been identified as highly selective (27000-fold), orally active ET<sub>B</sub> antagonist [104].

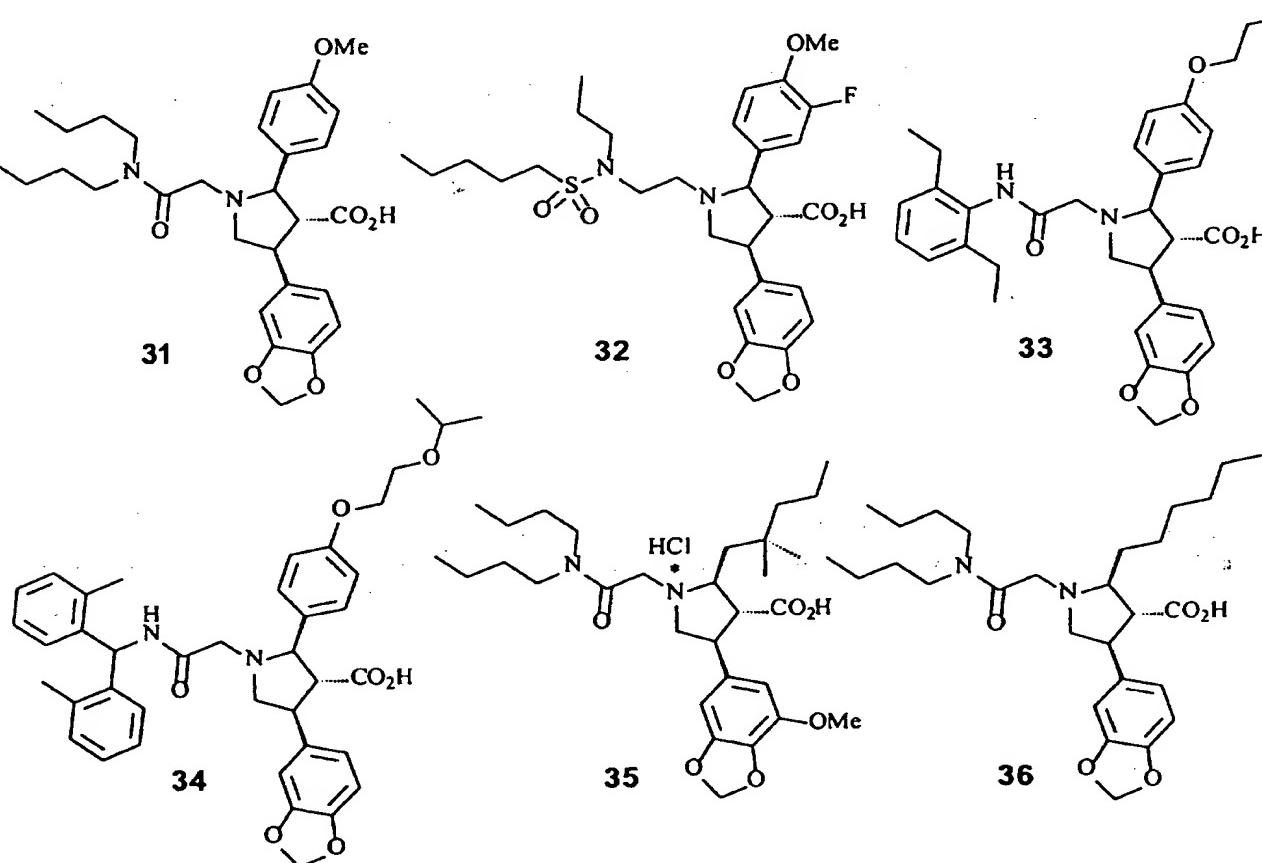


Fig. (13). Pyrrolidine carboxylic acid-type ET antagonists.

Administration of ET<sub>B</sub>-selective antagonist led to hypertensive responses indicating that they are not suitable as agents for a long-term systemic single ET<sub>B</sub>-directed therapy [103]. Nevertheless, ET<sub>B</sub>-selective antagonists are expected to be a valuable tool for the elucidation of the role of the ET<sub>B</sub> receptor action under normal and pathophysiological conditions [104]. Most recently, an ET<sub>A</sub>-selective antagonist, derived by optimization of A-127722 rac-31, emerged from the series of pyrrolidine-based compounds [105]. A-216546 35 is a further orally active ET receptor antagonist showing >25000-fold selectivity for the ET<sub>A</sub> receptor ( $K_i=0.46$  nM), and is considered for clinical development as a therapeutic agent for chronic treatment of ET-1-mediated diseases [106]. Compound 36 ( $IC_{50}=5.6$  nM (ET<sub>A</sub>); >10000-fold selectivity) is currently under investigation at Abbott's Laboratories as ET<sub>A</sub> antagonist. Apart from the ET receptor affinity, A-216546 35 showed remarkable inhibition potential for numerous members of the GPCR superfamily such as adenosine receptors,  $\delta$ -opioid receptor, purinergic receptor, etc. [106], thus indicating a kind of "ligand crosstalk" which turns out to be a common phenomenon of GPCR-targeted compounds.

#### Phenylacetamides

L-749,329 37 (Fig. (14)) is an orally active, competitive and nonselective ET<sub>A</sub>/ET<sub>B</sub> antagonist developed by Merck inhibiting the binding of [<sup>125</sup>I]ET-1 in Chinese Hamster Ovary (CHO) cells expressing human ET receptors with IC<sub>50</sub> values of 0.8 nM (ET<sub>A</sub>) and 16 nM (ET<sub>B</sub>), respectively [107]. The active enantiomer, L-754,142 37, is a potent orally active ET antagonist with a long duration of action in several *in vivo* models. L-754,142 37 shows binding affinity

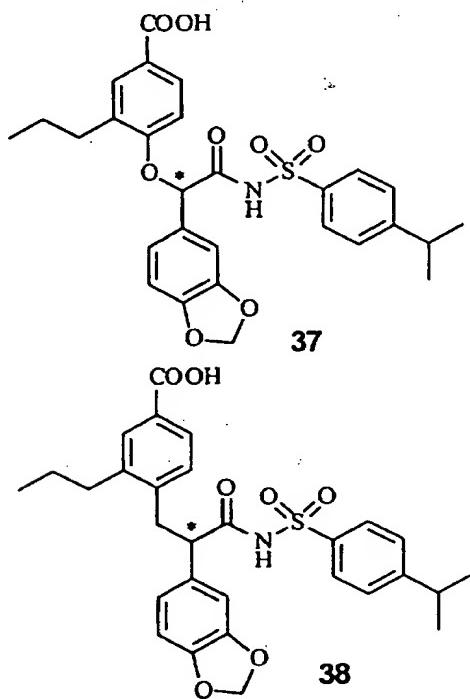


Fig. (14). Phenylacetamide-type ET antagonists.

towards ET<sub>A</sub> (0.062 nM) and ET<sub>B</sub> (2.25 nM) and antagonizes ET-1-induced phosphatidyl inositol hydrolysis in CHO cells expressing cloned human ET receptors with IC<sub>50</sub> values of 0.35 nM (ET<sub>A</sub>) and 26 nM (ET<sub>B</sub>) [108]. Substitution of the ether oxygen against a methylene group resulted in L-751,281 38, an analogue with similar activities on both ET receptor subtypes [107].

#### $\alpha$ -Phenoxyphenylacetic Acids

At the Merck laboratories, structural modifications of an initial lead discovered by screening for angiotensin II (All) antagonists, led to a dual AT<sub>1</sub>/ET antagonist. Further optimization towards ET<sub>A</sub>-selectivity resulted in L-744,453 39 (Fig. (15)), an  $\alpha$ -phenoxyphenylacetic acid derivative lacking the sulfonamide present in the arylacylsulfonamides L-749,329 37, and L-751-281 38 [107]. L-744,453 39 competitively and reversibly inhibits [<sup>125</sup>I]ET-1 binding to CHO cells expressing cloned human ET receptors with  $K_i$  values of 4.3 nM (ET<sub>A</sub>), and 232 nM (ET<sub>B</sub>). Thus, within L-744,453 39 the shift from an originally angiotensin II antagonist to an ET-selective antagonist could be demonstrated, thus highlighting the potential of "cross-fertilization" of projects devoted to representatives of a common receptor superfamily.

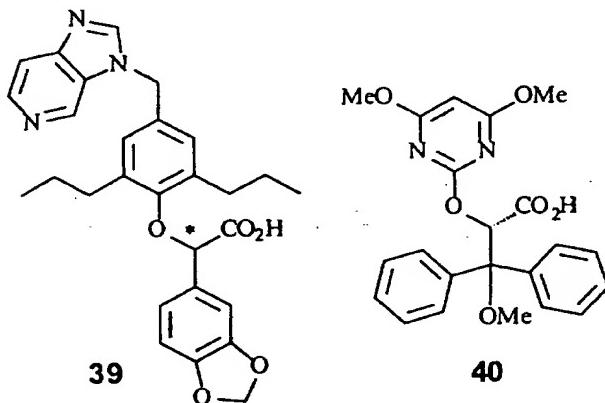


Fig. (15). Aryloxyacetic acid-type ET antagonists.

#### $\alpha$ -Aryloxyacetic Acids

Also at the BASF laboratories, the endothelin project started with screening of the in-house chemical substance stock. The initial lead, which was originally intended as a herbicide, was optimized by systematic structural modifications resulting in an ET<sub>A</sub>-selective antagonist, LU135252 40 (Fig. (15)), the active (S)-configured enantiomer of LU127043 [109,110]. It selectively binds to the ET<sub>A</sub> receptor with high affinity ( $K_i=2$  nM (ET<sub>A</sub>),  $K_i=184$  nM (ET<sub>B</sub>)) [111]. LU135252 40 has been evaluated in clinical trials for preventing restenosis [87] and entered phase II for CHF [112]. Furthermore, it was demonstrated that selective ET<sub>A</sub> receptor inhibition with LU135252 40 could reduce ischemia-induced ventricular arrhythmias in pigs. Thus ET antagonism might reduce mortality by preventing arrhythmias, a major cause of death in CHF, obviously induced by the pro-arrhythmic effects of ET-1 [100].

Phenoxybutanoic Acids and Stilbene acids

According to a previously elaborated SAR study, Astles *et al.* at Rhône-Poulenc Rorer presented the optimized analogue RPR-111844 41 (Fig. (16)), which exhibits an IC<sub>50</sub> of 5.0 nM at the rat ET<sub>A</sub> receptor and 1000-fold selectivity over the ET<sub>B</sub> receptor. The promising pharmacokinetics in a rat model of ET-1-induced vasoconstriction rendered this RPR-111844 41 an ideal candidate to examine these effects in preclinical models of cardiovascular disease [113].

In order to shed light on the characteristics of the bioactive conformation, a new series of rigidified analogues of stilbene acids were designed based on the SAR derived from a series of the phenoxybutanoic acids. Thus, compound RPR-111723 42 was identified as the most potent analogue with an IC<sub>50</sub> of 80 nM. Although the stilbene series was not further developed, results from SAR will be back-transferred into the more interesting series of phenoxy butanoic acids [114].

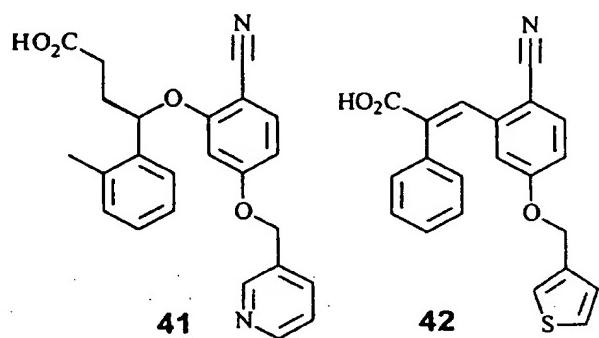


Fig. (16). Phenoxybutanoic acid- and stilbene acid-type ET antagonists.

**Bradykinin****Biomedical Significance**

The nonapeptide bradykinin (BK, Table 1), Arg-Pro-Pro-Gly-Phe-Ser-Pro-Phe-Arg, belongs to the family of kinins. Kinins are small peptides which are released from kinninogens by several enzymes, the kallikreins [115-120]. Interaction of BK with two designated receptor subtypes, B<sub>1</sub> and B<sub>2</sub>, results in a variety of biological effects including vasodilation, modulation of vascular permeability, smooth muscle contraction, recruitment and priming of inflammatory cells, induction of pain, modulation of transmitter release, stimulation of cell division, etc. [121]. Based on these diverse biological activities, BK is involved in inflammatory diseases, such as asthma, rhinitis, pancreatitis, sepsis, rheumatoid arthritis, brain oedema, and angioneurotic oedema [122]. Due to these pathophysiological actions of BK, mainly induced by the interaction with the B<sub>2</sub> receptor, this system emerged as an interesting target in pharmaceutical research. Hence, in a number of efforts BK antagonists were presented tempted to be a valuable tool in the treatment of above mentioned chronic diseases.

**Lead Finding****'Second-Generation' B<sub>2</sub> Antagonists**

Initiated by the discovery of NPC-567 by Vavrek and Stewart [123] in the 90's, a number of selective peptidic B<sub>2</sub> receptor antagonists including Icatibant (Hoe-140) [124,125] and Bradycor (Deltibant, CP-0127) [126], so-called 'second-generation' antagonists, have been clinically evaluated. In the following years, research programs were directed towards the discovery of B<sub>2</sub>-selective nonpeptide antagonists. Detailed overviews on this subject were provided only recently by Altamura *et al.* [127] and Heitsch [128] addressing projects of diverse research group, and reviewing the current patent situation.

In 1993, the naphthylalanine derivative WIN-64338 43 (Fig. (17)) was disclosed as the first nonpeptide B<sub>2</sub> antagonist [129,130]. A random screening approach at Sterling Winthrop led after optimization to compound WIN-64338 43, displaying a K<sub>i</sub> value of 64 nM for the inhibition of [<sup>3</sup>H]BK binding to the B<sub>2</sub> receptor (IMR-90 cells, fetal lung fibroblast cell line expressing the kinin B<sub>2</sub> receptor). However, this compound is problematic in terms of potency, oral bioavailability, and selectivity [130], since significant affinity for e.g. the muscarinic receptors was detected [131].

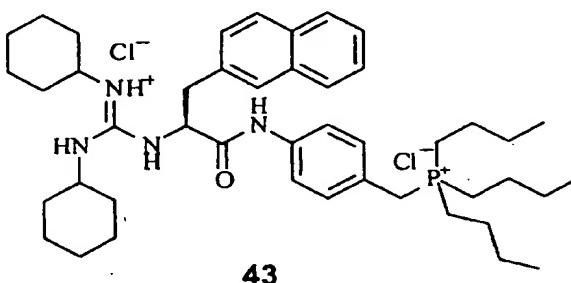


Fig. (17). 'Second-generation' B<sub>2</sub> antagonists WIN64338.

**'Third-Generation' B<sub>2</sub> Antagonists**

From 1994 on Fujisawa published a series of patent applications on new classes of potent, selective and orally active nonpeptide B<sub>2</sub> receptor antagonists [132-135], thereby establishing the so-called 'third-generation' compounds. Several derivatives showed nanomolar affinity in receptor binding assays and high efficacy in various species including humans. They also exhibited *in vivo* functional antagonistic activity against BK-induced bronchoconstriction in guinea pigs and potency in diverse animal models of inflammation [132-135] [136,137]. Again, these compounds originally emerged from a random screening directed towards the angiotensin II (AT<sub>1</sub>) receptor and belong to a class of imidazo[1,2-a]pyridines. A detailed description of the design, synthesis and biological evaluation was given by Kayakiri *et al.*, only recently [138]. The first lead compound 44 (Fig. (18)) of this series of N-containing heteroaromatic benzyl ethers showed an IC<sub>50</sub> value of 7.6 μM.

Within a classical medicinal chemistry approach based on SAR considerations the first lead compound 44 was exposed to extensive modifications leading to 45 (Fig. (18)).

This analogue displays an  $IC_{50}$  value of 2.4 nM for the inhibition of the specific binding of [ $^3$ H]BK to B<sub>2</sub> receptors in guinea pig ileum (GPI) membrane preparations. Thus, the 8-[3-(N-acylglycyl-N-methylamino)-2,6-dichlorobenzyl]oxy-3-halo-2-methylimidazo[1,2-*a*]pyridine skeleton was identified as the basic framework of the first orally active nonpeptide B<sub>2</sub> antagonist. In order to overcome species difference, further modifications within the 3-position of the benzyl moiety revealed an analogue (FR167344 46) exhibiting subnanomolar ( $IC_{50}$ =0.66 nM) and low nanomolar binding affinities ( $IC_{50}$ =1.4 nM) for GPI membrane and human A431 cells (epidermoid carcinoma cells) [136,139], respectively.

Recent results indicate that FR167344 46 has specific antagonistic activity against guinea pig tracheal smooth muscle BK receptors, thus rendering it a potential therapeutic tool for the treatment of asthma [140]. Derivatives containing the *N,N*-dimethylcarbamoyl-

substituted cinnamide group were capable of overcoming species differences, and therefore defined the required pharmacophore for further investigations. FR167344 46 was assigned as new lead compound for three independent optimization approaches implying substitutions within the imidazo[1,2-*a*]pyridine moiety (benzimidazoles, quinoxalines, and quinolines). While further optimization of the quinoxaline series failed, optimization within the benzimidazole and quinoline series resulted in several potent congeners. Thus, consequent SAR studies of the benzimidazoles afforded improvements of *in vivo* oral activities, resulting in FR185627 47 which exhibits 75.2 % inhibition against BK-induced bronchoconstriction at 0.32 mg/kg, *i.p.* [138]. Optimization of the quinoline series afforded compound FR173657 48 with high potency in B<sub>2</sub> binding affinities for both GPI ( $IC_{50}$ =0.46 nM) and human recombinant B<sub>2</sub> receptors ( $IC_{50}$ =1.4 nM) [136,141]. FR173657 48 displays the best *in vivo* B<sub>2</sub> antagonistic oral activity among nonpeptide antagonists investigated so far

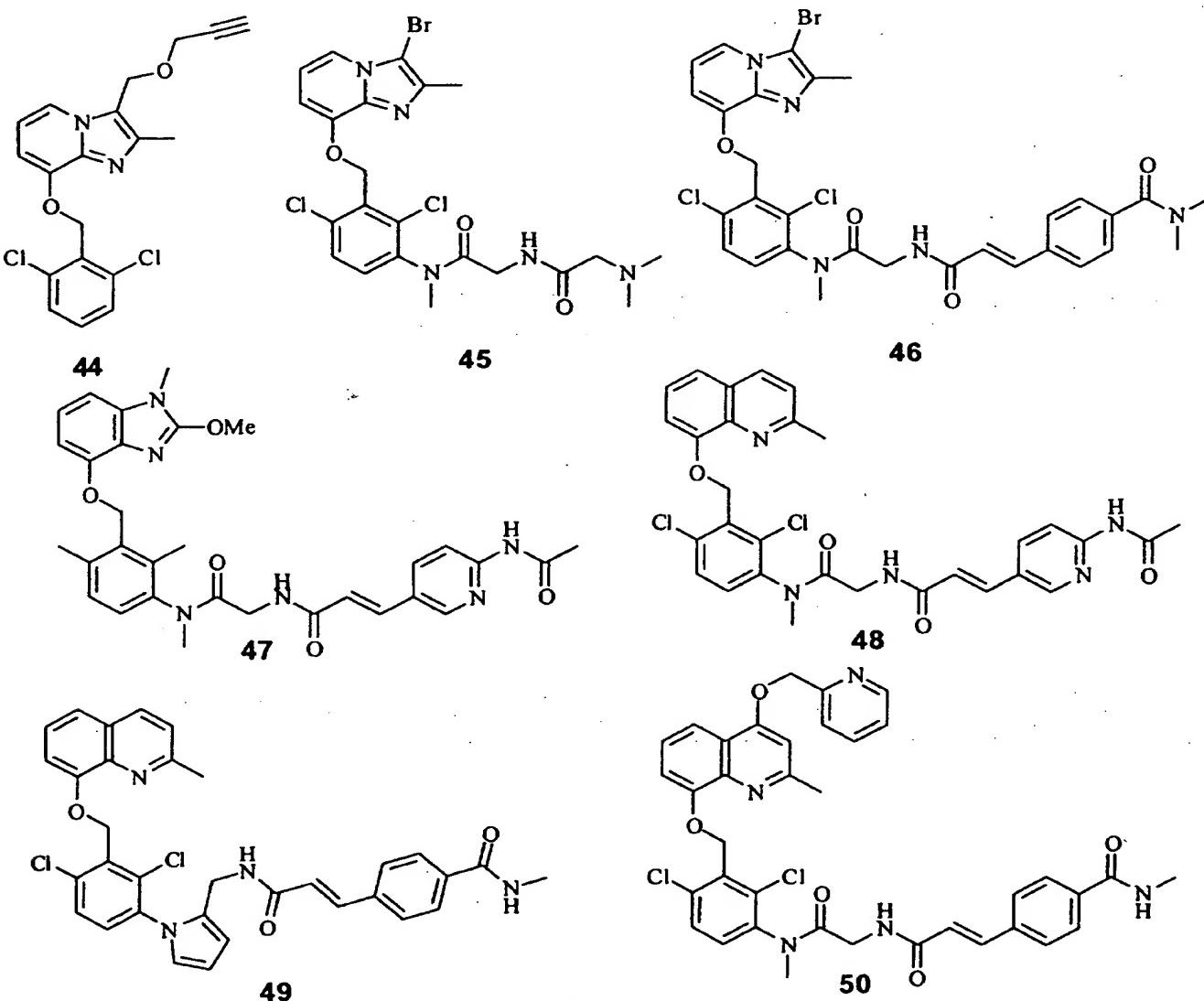


Fig. (18). 'Third-generation' B<sub>2</sub> antagonists developed by Fujisawa.

and was chosen as a clinical candidate for the treatment of various inflammatory diseases. Recent investigations on plasma extravasation mediated by activation of sensory nerves in guinea pig airways suggest FR173657 48 to be an orally active, promising anti-inflammatory agent for kinin-independent inflammation following antigen challenge [142]. Fujisawa researchers further report on the postulation of the active conformation of their compounds by synthesizing conformationally restrained analogues. Molecular modelling studies and subsequent chemical synthesis of a novel pyrrole series afforded FR193144 49, an analogue which mimics the previously postulated *cis*-conformation of the *N*-methylamide by the pyrrole moiety. FR193144 49 exhibits excellent binding affinity for human recombinant B<sub>2</sub> receptors ( $IC_{50}=0.26$  nM), thereby proving the *cis*-conformation as the bioactive conformation of the *N*-methylamide bearing antagonists (Fig. (18)) [138].

Interestingly, only minor variations within the core structure of the B<sub>2</sub> antagonists resulted in an analogue, FR190997 50 (Fig. (18)), exhibiting an agonistic profile [143]. The agonistic behaviour is hypothesized to be encoded in the difference concerning the 4-substituent of the quinoline moiety within the agonist compared to the antagonists (H  $\leftrightarrow$  2-pyridylmethoxy). FR190997 50 induces hypotensive response in anaesthetized rats and thus, is claimed for the treatment of hypertension, renal failure, heart failure, circulatory disorders, angina, restenosis, hepatitis etc [143].

#### B<sub>2</sub> Antagonists Structurally Related to FR173657

Compounds evaluated at Fournier are structurally related to Fujisawa's quinoline series differing mainly in the substituent in 3-position of the benzene-linkage which is replaced by a sulfonamide. LF16-0335 51 (Fig. (19)) is a potent, selective and competitive antagonist of the human B<sub>2</sub> receptor, displacing [<sup>3</sup>H]BK binding to membrane preparations of CHO cells expressing cloned human B<sub>2</sub> receptors with a  $K_i$  value of 0.84 nM.

LF16-0335 51 shows neither affinity for the B<sub>1</sub> receptor, nor binds significantly to any other membrane receptor except the muscarinic M2 ( $IC_{50}=0.9$   $\mu$ M) and M1 ( $IC_{50}=1.0$   $\mu$ M) receptors [144]. The hydrochloride of this derivative,

LF16-0335C, inhibits competitively BK-induced contractions of isolated rat uterus and GPI in functional assays [145]. Given i.v., LF16-0335C inhibits BK-induced hypotension in both animal species in a dose-dependent manner [145]. Substitution of the piperazine ring in LF16-0335 51 against a diaminopropane unit led to LF16-0687 52 (Fig. (19)) which was shown in competition binding studies with [<sup>3</sup>H]BK to bind to the human recombinant B<sub>2</sub> receptor expressed on CHO cells with an  $K_i$  value of 0.67 nM (LF16-0335 51,  $K_i=0.84$  nM). It functions as a competitive antagonist of BK-mediated contractions in isolated organs, i.e. rat uterus and GPI. Contrary to LF16-0335 51, LF16-0687 52 showed selectivity for the B<sub>2</sub> receptor in binding and functional studies performed on more than 40 different receptors.

In a new series of patent applications, Hoechst claimed a number of derivatives based on the lead structures delineated by Fujisawa as potent B<sub>2</sub> receptor antagonists. These heteroarylbenzyl ethers belong to a series of *O*-substituted 8-quinolines or 4-benzothiazoles [146]. Heitsch *et al.* report that the potency of the quinoline series was found to be higher compared to the corresponding benzothiazoles. The most potent antagonist 53 (Fig. (20)) shows an  $IC_{50}$  value of 0.7 nM for the inhibition of specific binding of [<sup>3</sup>H]BK to GPI membrane preparations and an  $EC_{50}$  value of 4.1 nM for the inhibition of BK-induced contraction of isolated GPI.

The most potent corresponding antagonist of the benzothiazole series 54 (Fig. (20)) exhibits an  $IC_{50}$  value of 10.3 nM and an  $EC_{50}$  value of 54 nM. Another representative example of the B<sub>2</sub> antagonist claimed by Hoechst is compound 55 (Fig. (20)) which incorporates a 2-aminoethanol unit instead of the *N*-methylamide as linker in the central part of the molecule. 55 inhibits [<sup>3</sup>H]BK binding (GPI) with a  $K_i$  value of 20 nM [127,128].

Based on the template FR173657 48, Kyowa Hakko filed a patent application claiming heteroarylbenzyl ethers as B<sub>2</sub> antagonists [147]. Like in FR173657 48, the central ether entity is flanked by a terminal quinoline and a dichlorobenzene linker. Instead of the classical *N*-methylamide sidechain in 3 position, the dichlorobenzene linker bears a branched hydrocarbon chain (56, Fig. (20)).

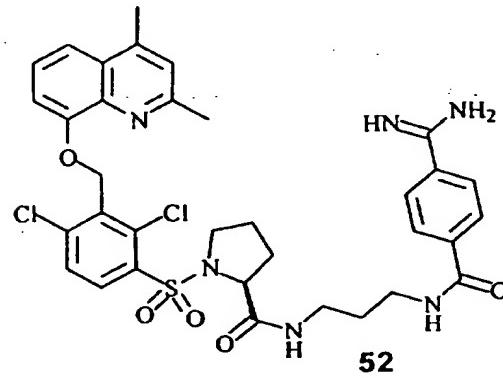
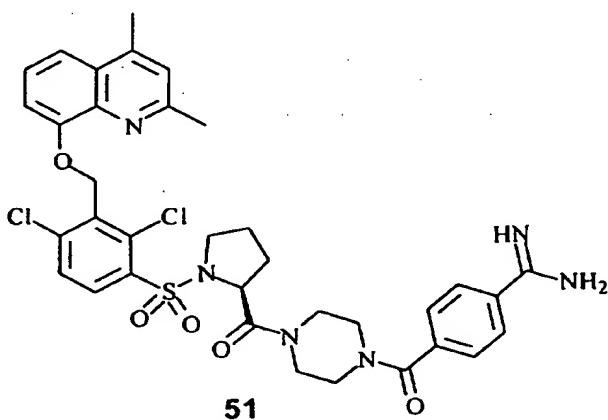
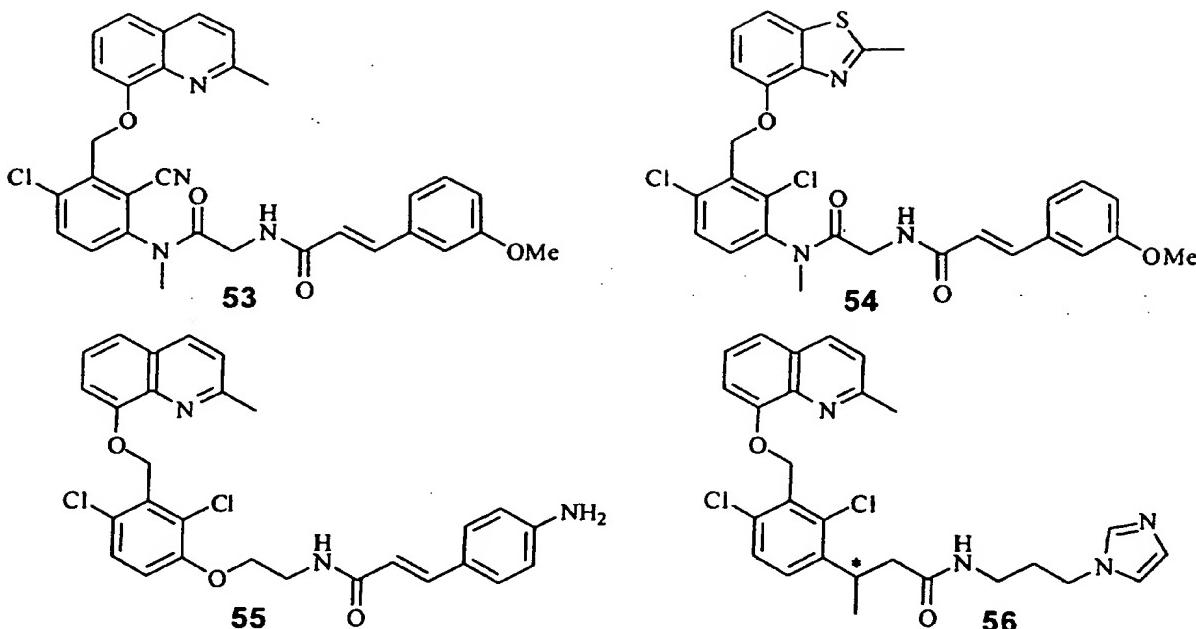


Fig. (19). B<sub>2</sub> receptor antagonists disclosed by Fournier.

Fig. (20). Miscellaneous heteroarylbenzylether-type B<sub>2</sub> antagonists.Miscellaneous Nonpeptide B<sub>2</sub> Antagonists

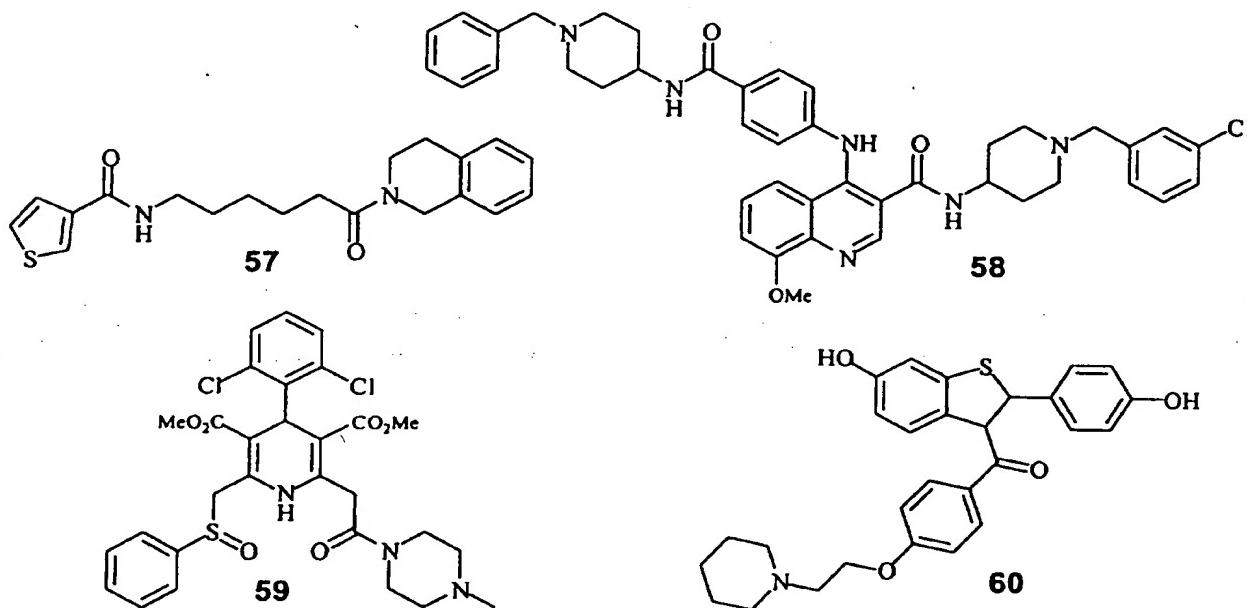
From screening of a 4000 compound combinatorial library, GlaxoWellcome found a promising tetrahydroisoquinoline, GR213548X 57 (Fig. (21)), with affinity for the B<sub>2</sub> receptor in the micromolar range [127].

Further B<sub>2</sub> antagonists are claimed in a series of patent applications by a number of companies. American Home Products (AHP, Wyeth Ayerst) presented compound 58 which structurally resembles the Fujisawa derivatives only with respect to a quinoline entity. Pfizer described 1,4-

dihydropyridines such as 59 to act as B<sub>2</sub> antagonists, while Eli Lilly disclosed benzothiophenes 60 (Fig. (21)) [127,148-150].

**Neurokinin***Biomedical Significance*

Neurokinins (NKS), also termed tachykinins belong to a family of peptides sharing a common homologous C-terminal fragment composed of the pentapeptide amide Phe-

Fig. (21). Miscellaneous B<sub>2</sub> antagonists.

Xaa-Gly-Leu-Met-NH<sub>2</sub> (Table 1) [151]. The interaction of substance P (SP), neuropeptide A (NKA), and neuropeptide B (NKB) with their corresponding receptors [152], notably NK<sub>1</sub>, NK<sub>2</sub>, and NK<sub>3</sub> plays a pivotal role in induction and progression of inflammatory diseases. Neuropeptide interaction is involved in a variety of physiological and pathophysiological conditions such as pain, inflammation, smooth muscle contraction, vasodilation, and activation of the immune system. Thus, NK receptor antagonists emerged as interesting agents for the treatment of primarily pain, emesis and asthma but also to interfere in other disorders such as anxiety, arthritis, migraine, cancer and schizophrenia [153-156]. NK receptor antagonists have been reviewed e.g. by Elliot and Seward [157], von Sprecher *et al.* [158], and, only recently, in *Current Medicinal Chemistry* by Gao and Peet [159]. Therefore, this contribution will solely focus on nonpeptide NK antagonists.

## Lead Finding

### NK<sub>1</sub> Antagonists

The quinuclidine-based analogue CP-96,345 61 (Fig. (22)) was developed from a lead structure found by random screening and is the first nonpeptide NK<sub>1</sub>-selective antagonist showing an IC<sub>50</sub> value of 0.77 nM (lymphoblast M-9 cells) [160]. Over the last years, CP-96,345 61 evolved as the main pharmacological tool in the area of NK receptor research.

A second series of piperidine-containing analogues developed at Pfizer includes CP-99,994 62 [161] and CP-122,721 63 (Fig. (22)) [162]. CP-99,994 62 exhibits analgesic efficacy [163] and shows less *in vivo* inhibition of NK<sub>1</sub> receptor-mediated responses compared to the 5-trifluoromethoxy analogue, CP-122,721 63 [164]. The latter

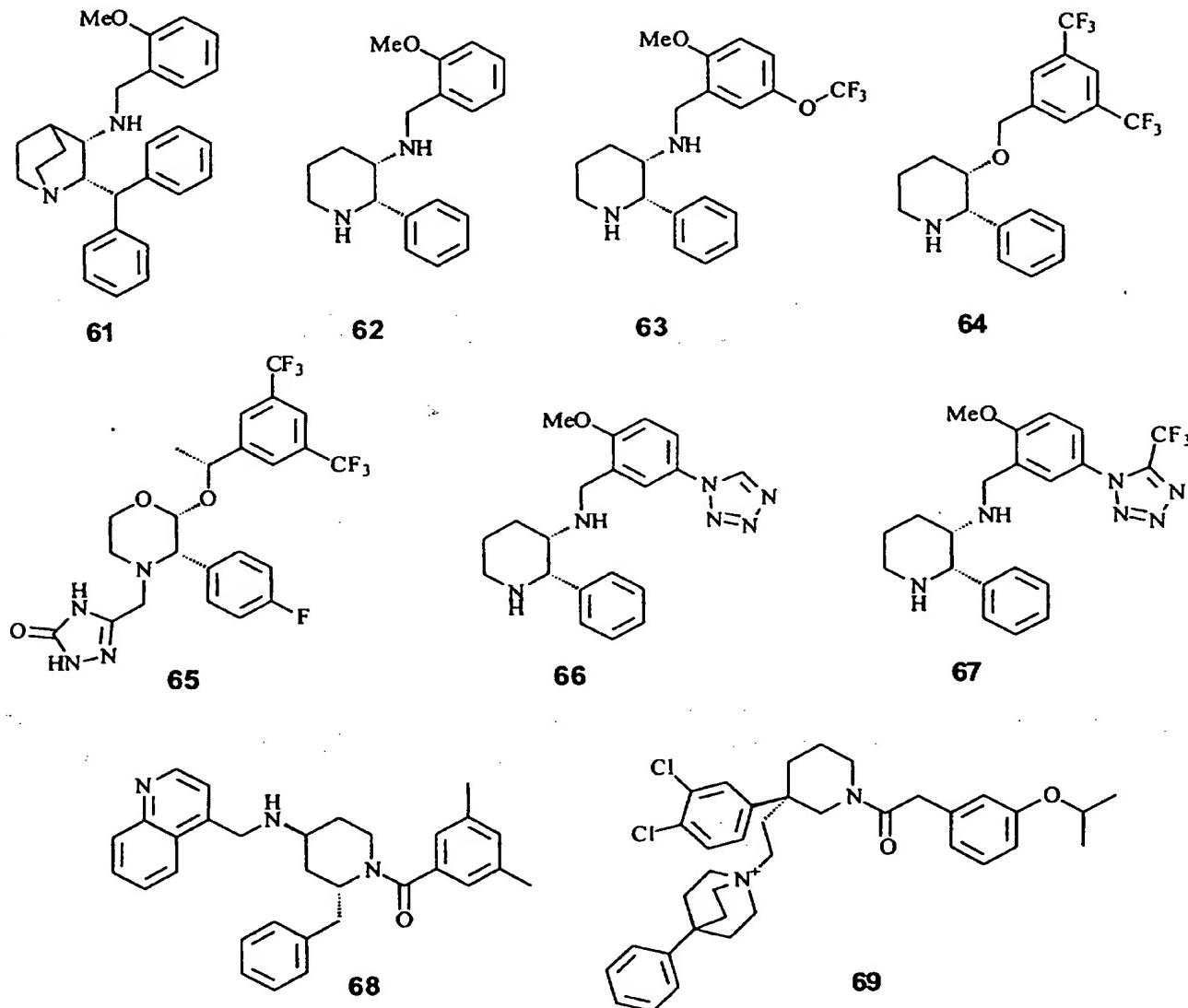


Fig. (22). Quinuclidine-, piperidine-, and morpholine-derived NK<sub>1</sub> antagonists.

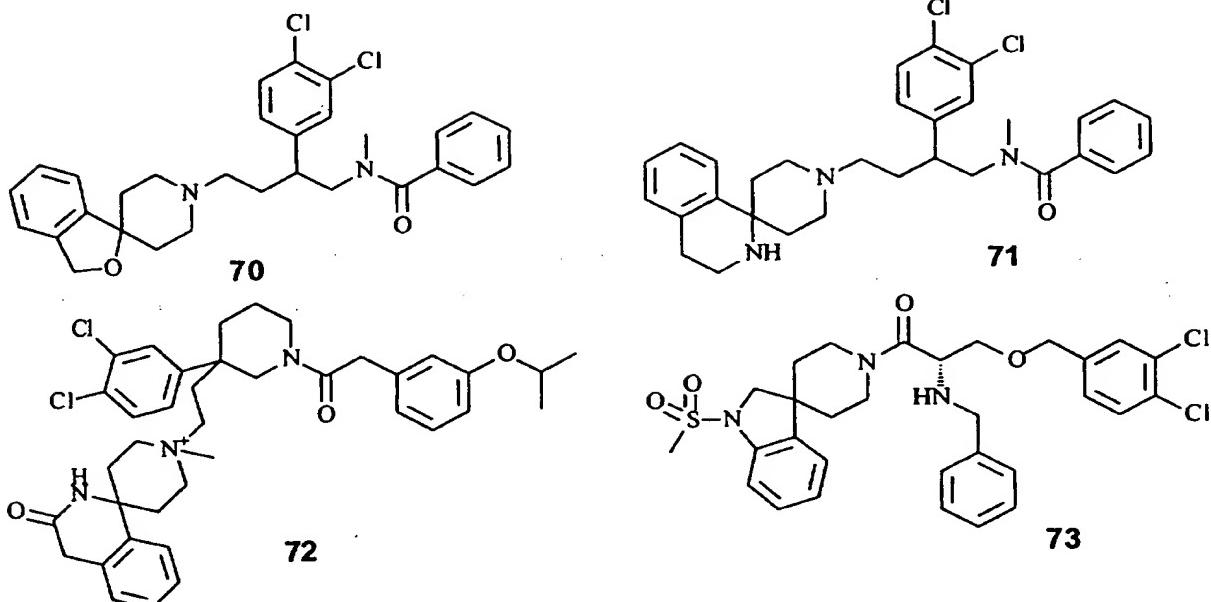


Fig. (23). Spiro-aryl piperidine-type NK<sub>1</sub> antagonists.

congener shows improved antiemetic properties in acute cisplatin-induced vomiting in tumor patients when administered in combination with a 5-HT<sub>3</sub> antagonist [157].

Based on the piperidine core structure of CP-99,994 62, Merck synthesized L-733,060 64 ( $IC_{50}=0.87$  nM in CHO cells) [165] which, after modifications, led to the metabolically more stable L-754,030 65 ( $IC_{50}=0.1$  nM in CHO cells) (Fig. (22)) [166]. Recent results indicate that L-754,030 65 prevents cisplatin-induced emesis in patients receiving an anticancer chemotherapy [167,168].

Glaxo disclosed the 5-tetrazolyl-substituted analogue GR-203,040 66 (Fig. (22)) retaining the piperidine core structure of CP-99,994 62 as NK<sub>1</sub> antagonist (GR-203,040 66:  $pK_i=10.3$  nM in CHO cells) which was selected for clinical evaluation in emesis and migraine [169,170]. Further modification revealed GR-205,171 67 (Fig. (22)) ( $pK_i=10.6$  nM in CHO cells) which, apart from oral bioavailability, exhibits also reduced L-type calcium channel activity, a side effect associated with e.g. CP-122,721 63. GR-203,040 66 ameliorates tissue damage induced by x-irradiation or cisplatin [171,172].

Novartis developed CPG-49,823 68 (Fig. (22)), based on the piperidine scaffold for anxiety-related indications [173]. CPG-49,823 68 ( $IC_{50}=12$  nM, bovine retina) has been tested for its antagonistic potential against the depolarization of spinal motoneurones by bath application of the selective tachykinin receptor against septide(6-11) exhibiting an  $IC_{50}$  value of 0.3  $\mu$ M (gerbil preparations) and 7.8  $\mu$ M (rat preparations) [174].

The central piperidine unit is also found in the Sanofi compound SR-140,333 69 (Fig. (22)) ( $IC_{50}=0.01$  nM in IM-9 cells), also termed Nolpitantium, which emerged from a random screening approach followed by a lead optimization program [175].

Investigations on the effects of SR-140,333 69 on nociceptive pathways in rats revealed this agent to be a potent drug for pain relief [176]. Kubota *et al.* reported on the synthesis of spiro-piperidines as NK<sub>1</sub> receptor antagonists [177]. SAR studies starting from the primary lead YM-35375 70 (dual NK<sub>1</sub>/NK<sub>2</sub> antagonist) (Fig. (23)) yielded analogue YM-35384 71 as a selective NK<sub>1</sub> antagonist which was 12-fold more potent compared to the original spiro-isobenzofuran-1(3H)-4'-piperidine YM-35375 70. YM-35384 71 already showed an  $IC_{50}$  value of 58 nM which could be improved by further modification resulting in compound YM-49244 72 (Fig. (23)), a spiro-substituted piperidinium salt with an  $IC_{50}$  value of 1.9 nM against SP-induced contraction in guinea pig ileum and inhibitory activity against selective NK<sub>1</sub> receptor agonist-induced bronchoconstriction in guinea pigs ( $ID_{50}=24$   $\mu$ g/kg, i.v.) [177].

A further class of spiro-aryl piperidines is represented by Merck Sharp and Dohme's spirocyclic aryl sulfonamides, serine-derived NK<sub>1</sub> antagonists [178]. Compound 73 (Fig. (23)) exhibits an  $IC_{50}$  value of 1.0 nM for the displacement of [<sup>125</sup>I]SP from NK<sub>1</sub> receptors in CHO cells and served for

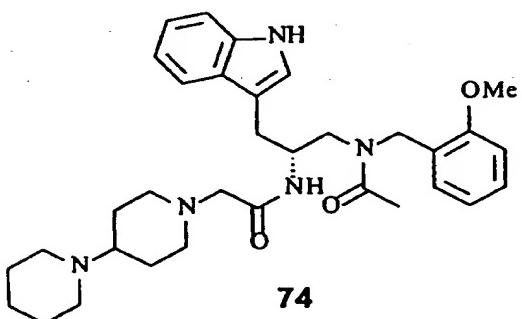


Fig. (24). Lanepitant disclosed by Eli Lilly.

the development of a pharmacophore model for the receptor binding requirements [179].

Eli Lilly has identified the tryptophane-derived LY-303,870 74 (Fig. (24)) as a selective antagonist binding to NK<sub>1</sub> with high affinity, while lacking ion channel activity [180]. LY-303,870, Lanepitant 74, is a candidate for clinical development in animal models of inflammation, pain, migraine, and asthma [158].

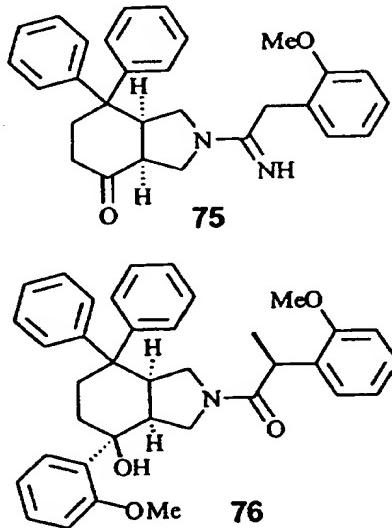


Fig. (25). Perhydroisoindole-type NK<sub>1</sub> antagonists.

RP-67,580 75 (Fig. (25)) emerged after lead optimization of an initial screening hit of Rhône-Poulenc Rorer's compound library. RP-67,580 75 belongs to a class of substituted perhydroisoindoles which, apart from poor oral bioavailability, also suffered from L-type calcium channel interaction [151,181]. The follow-up compound RPR-

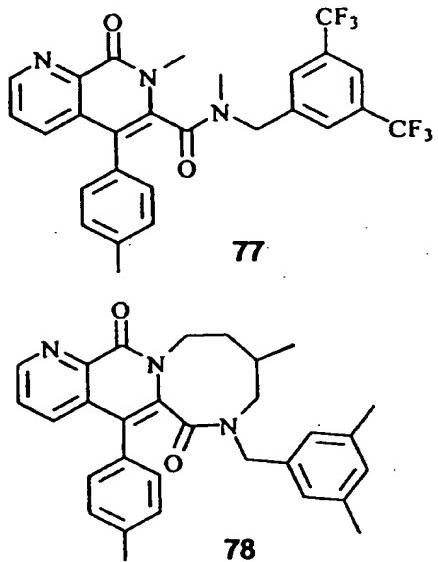


Fig. (26). Naphthydine-type NK<sub>1</sub> antagonists.

100,893 76 (Fig. (25)), Dapitan, exhibits superior binding affinity ( $IC_{50}=13$  nM, IM-9 cells) [182].

Investigations of the axially chiral 1,7-naphthydine-6-carboxamide 77 (Fig. (26)) revealed that the atropisomer (*aR*)-trans-77 represents the bioactive receptor-bound conformation of this potent NK<sub>1</sub> antagonist [183]. This analogue exhibits *in vitro* antagonistic activities for the inhibition of [<sup>125</sup>I]Bolton-Hunter(BH)-SP binding in human lymphoblast cells (IM-9) with an  $IC_{50}$  value of 0.24 nM. Further, it shows *in vivo* potency by inhibiting capsaicin-induced plasma extravasation in the trachea of guinea pigs upon *i.v.* and *p.o.* administration.

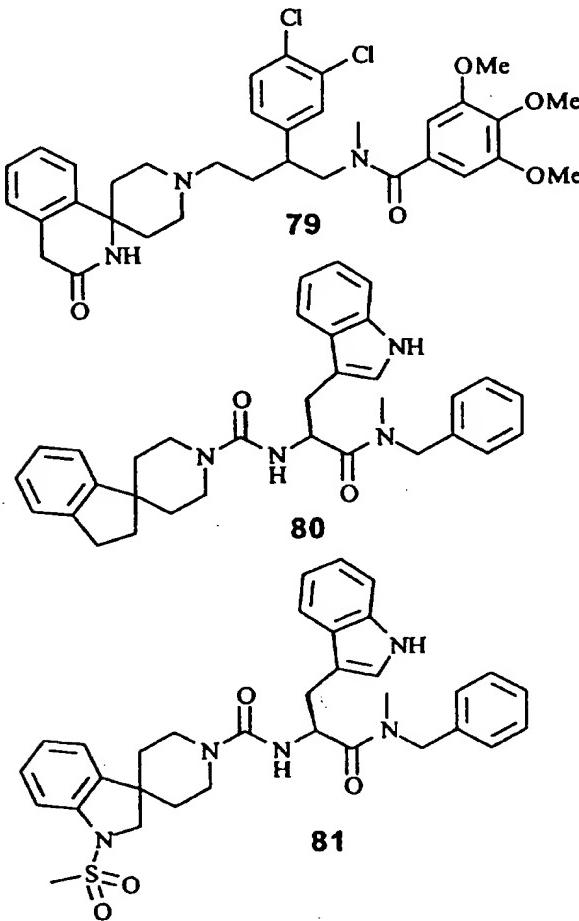
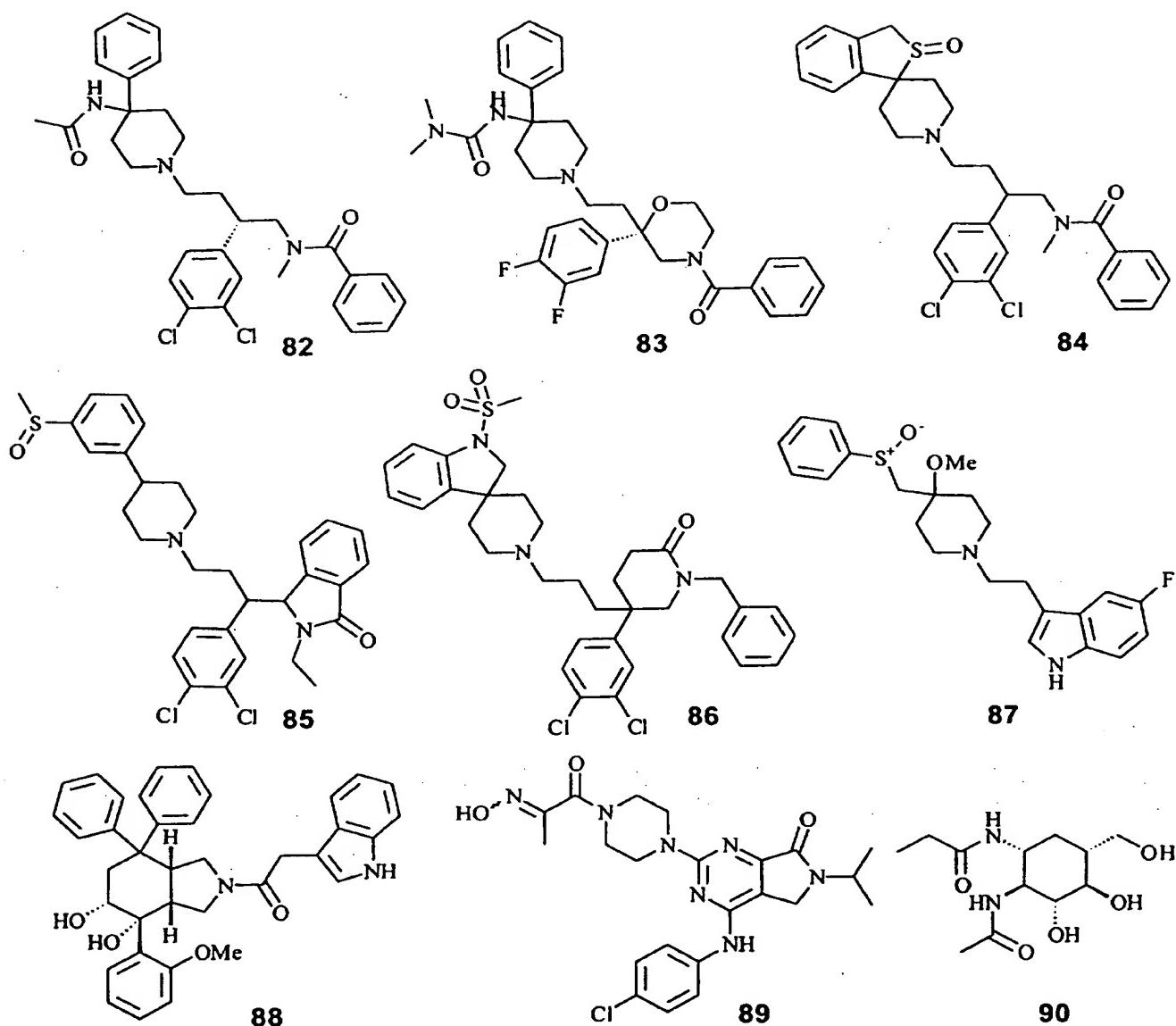


Fig. (27). Dual NK<sub>1</sub>/NK<sub>2</sub> antagonists.

Based on this template, Natsugari *et al.* [183] developed TAK-637 78 (Fig. (26)), the (*aR,9R*)-atropisomer of a cyclic naphthyridine analogue. TAK-637 78 exhibits an  $IC_{50}$  value of 0.45 nM, an  $ID_{50}$  of 4.3  $\mu$ g/kg and 33  $\mu$ g/kg after *i.v.* and *p.o.* administration, respectively. Further it increased the shutdown time of distension-induced bladder contractions and the bladder volume threshold in guinea pigs, thus implying its clinical potential in the treatment of pollakiuria and urinary incontinence [183]. The x-ray structures of 77 and 78 provide insights in the prerequisite structural



**Fig. (28).** NK<sub>2</sub> antagonists.

requirements for NK<sub>1</sub> receptor binding, thereby assigning the (*αR,9R*)-isomer as the active conformation [183].

#### Dual NK<sub>1</sub>/NK<sub>2</sub> Antagonists

Since the release of SP and NKA causes mucus secretion, airway constriction, and plasma extravasation - typical clinical symptoms of asthma - it has been suggested to use dual NK<sub>1</sub>/NK<sub>2</sub> antagonists in the treatment of asthma [184].

Considering the structural requirements of Sanofi's NK<sub>2</sub>-selective antagonist SR-48968 82 (Fig. (28), see below), researchers at Yamanouchi Pharm. developed the spiro[isobenzofuran]piperidine YM-35375 70 (Fig. (23)) with binding affinity towards the NK<sub>2</sub> receptor with an IC<sub>50</sub> value of 84 nM and an IC<sub>50</sub> value 710 nM for NK<sub>1</sub>, respectively. Further, it shows inhibitory activity (ID<sub>50</sub>=41

μg/kg, i.v.) against [ $\beta$ -Ala<sup>8</sup>]NKA(4-10)-induced bronchoconstriction in guinea pigs [185]. Utilizing this new NK<sub>1</sub>/NK<sub>2</sub> dual antagonist as lead compound a further spiro-substituted piperidine analogue, YM-44778 79 (Fig. (27)), was developed, exhibiting potent antagonistic activities against the NK<sub>1</sub> (IC<sub>50</sub>=82 nM) and NK<sub>2</sub> (IC<sub>50</sub>=62 nM) receptors in isolated tissues [185], respectively.

Based on L-tryptophanebenzyl esters, Qi *et al.* reported on the synthesis of two compounds 80, and 81 with dual NK<sub>1</sub>/NK<sub>2</sub> receptor affinity (Fig. (27)) [186].

80 contains a 4-spiroindano piperidine and shows dual NK activity combined with slightly improved NK<sub>2</sub> activity (IC<sub>50</sub>=56 nM (hNK<sub>1</sub>), IC<sub>50</sub>=27 nM (hNK<sub>2</sub>)). Upon incorporation of a 4-spiroindolin sulfonamide, the balanced antagonist 81 was obtained (IC<sub>50</sub> = 14 nM - NK<sub>1</sub>; 24 nM - NK<sub>2</sub>).

**NK<sub>2</sub> Antagonists**

NK<sub>2</sub> antagonists are of particular interest for the treatment of chronic diseases such as asthma, inflammatory bowel disorders, rheumatoid arthritis, pain, emesis, and psychiatric disorders [157].

The first NK<sub>2</sub> antagonist, SR-48,968 82 (Fig. (28)), Saredutant, was described in 1992 [187]. This potent antagonist has been shown to inhibit the NKA-induced bronchoconstriction in isolated human airways. Only recently, a study of van Schoor *et al.* have demonstrated that NKA-induced bronchoconstriction in asthmatics was significantly reduced with 100 mg Saredutant administered *p.o* [188].

Based on this prototype compound, a number of analogues emerged from different laboratories. SR-144,190 83 (Fig. (28)) retains the phenylpiperidine moiety but contains an additional morpholine unit in order to introduce rigidity. Compared to the parent compound, it exhibits a similar pharmacological profile with increased bioavailability in the CNS [189].

Also Yamanouchi (YM-38336) 84 and Zeneca (ZD-7944) 85 (Fig. (28)) presented potent NK<sub>2</sub> antagonists based on the Sanofi lead structure (SR-48,968 82). ZD-7944 85 [190], showing a  $K_i$  value of 0.14 nM (MEL cells), still retains the phenylpiperidine entity, while YM-38336 84 [191] has been modified by introduction of a spiro-benzothiophene residue in position 4 of the piperidine. YM-38336 84 shows potent NK<sub>2</sub> inhibitory activity against [ $\beta$ -Ala<sup>8</sup>]NKA(4-10)-induced bronchoconstriction in guinea pigs, demonstrated by an ID<sub>50</sub> value of 20 mg/kg, *i.v.* [192].

Harrison *et al.* reported on the development of selective NK<sub>2</sub> and NK<sub>3</sub> antagonists based on a common structural

template, notably the NK<sub>3</sub>-selective compound SR-142,801 91 (Fig. (29), see below) [193]. Transfer of the carbonyl oxygen from an exocyclic to an endocyclic position on the piperidine ring led to two series of selective analogues, NK<sub>2</sub> and NK<sub>3</sub> antagonists, respectively [193]. An example of a potent NK<sub>2</sub> antagonist is given by compound 86 (Fig. (28)) which exhibits an IC<sub>50</sub> value of 2.2 nM for the displacement of [<sup>125</sup>I]NKA from the cloned human NK<sub>2</sub> receptor in CHO cells.

A number of preclinical nonpeptide NK<sub>2</sub> antagonists have been reported by GlaxoWellcome, Rhône-Poulenc Rorer and Zeneca, e.g. GR-159,897 87, RPR-106,145 88 (related to the NK<sub>1</sub> antagonist RPR-100,893 76, (Fig. (25))), and ZM-253,270 89 (Fig. (28)) [158], respectively.

Menarini used an interestingly rigid template for its selective NK<sub>2</sub> antagonists ( $K_i$ =2.5 nM) MEN-11420 90, Nepadutant, exhibiting improved *in vivo* potency and duration which is attributed to its rigid structure [194].

**NK<sub>1</sub> Antagonists**

The first selective nonpeptide NK<sub>3</sub> antagonist, SR-142,801 91, Osanetant, has been reported by Sanofi ( $K_i$ =0.21 nM, CHO cells) (Fig. (29)) [195].

Based on this structural template, Merck Sharp and Dohme elaborated a series of NK<sub>2</sub> and NK<sub>3</sub> antagonists, exemplified with analogue 92 (Fig. (29)), the corresponding congener of 86 (Fig. (28)).

SmithKline Beecham claimed NK<sub>3</sub> antagonists for the treatment of CNS diseases, pulmonary disorders and dermatitis [196]. Based on a quinoline core structure,

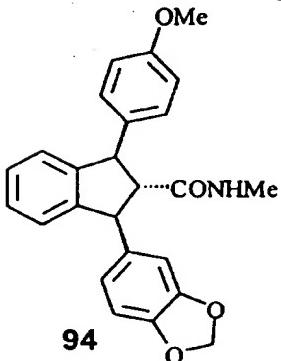
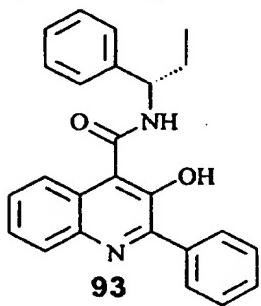
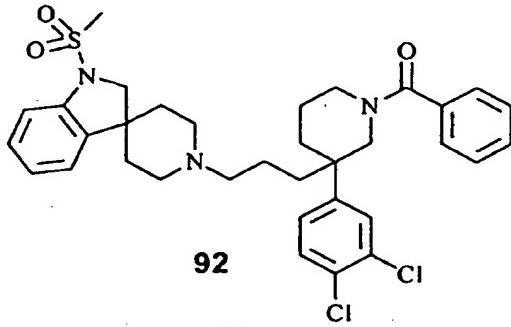
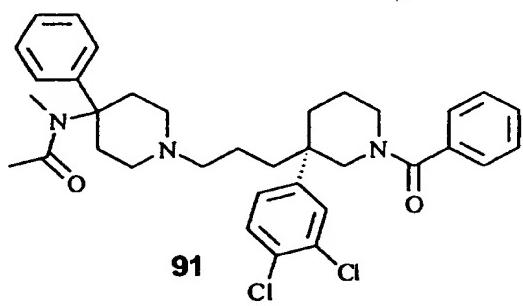


Fig. (29). NK<sub>3</sub> antagonists.

Giardina *et al.* developed SB-223,412 93 (Fig. (29)) demonstrating high NK<sub>3</sub> activity ( $IC_{50}=1.2$  nM,  $K_i=1.0$  nM, CHO cells), weak NK<sub>2</sub> activity, and no affinity for other receptors including ion channels [197]. SB-223,412 93 exhibits *in vitro* and *in vivo* oral and intravenous activity in animal models [198].

An entirely novel structure, 94 (Fig. (29)), has been claimed as NK<sub>3</sub> antagonist for the treatment of bronchitis, asthma, anxiety, Parkinson's disease and dermatitis [199]. Interestingly, this compound resembles strongly the indane carboxylic acids of SmithKline Beecham's ET antagonists.

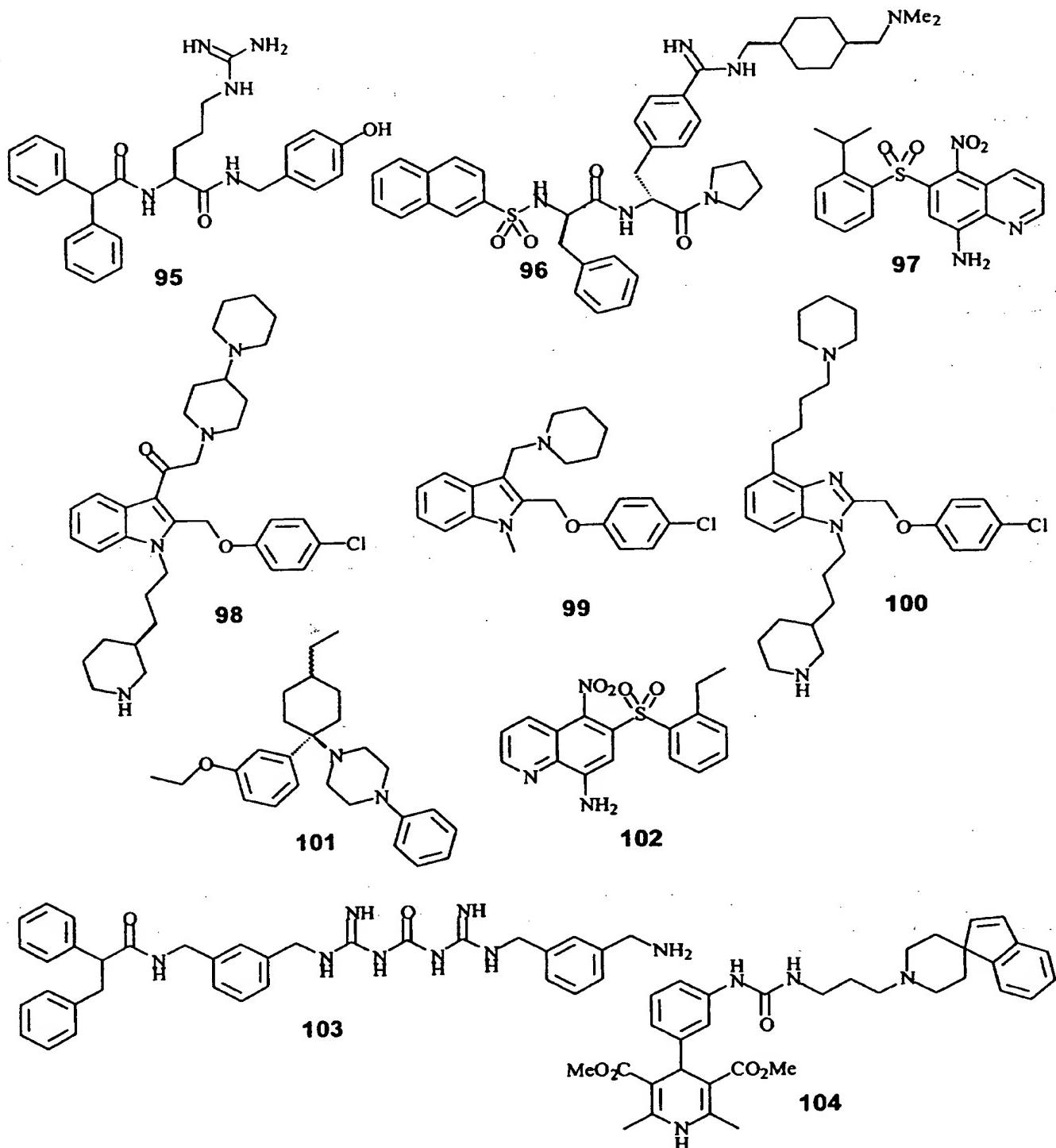


Fig. (30). Miscellaneous Y<sub>1</sub> antagonists.

**Neuropeptide Y****Biomedical Significance**

The 36-amino acid peptide neuropeptide Y (NPY, Table 1) was discovered in 1982 by Tatsumoto *et al.* [200]. NPY is a member of the pancreatic polypeptide family, also including structurally related peptide YY (PYY) and pancreatic peptide (PP) [201]. NPY is widely distributed throughout the mammalian central and peripheral nervous system [202,203]. Interacting with its at least six receptor subtypes ( $Y_1-Y_6$ ) it is involved in numerous physiological functions, e.g. food intake, blood pressure regulation, hormone secretion, sexual behaviour, and circadian rhythm [204-209]. Patent literature issued over the last ten years concentrate mainly on the inhibition of receptor-ligand interactions by low-molecular weight compounds in order to therapeutically interfere in mechanisms such as anxiety, appetite stimulation, obesity, alcohol intake, hypertension, and regulation of coronary tone [210]. As the  $Y_1$  and  $Y_5$  receptors are suggested to control feeding behaviour, they are believed to be the best target systems for developing antagonists as therapeutics for the treatment of obesity [204,211-213]. The  $Y_1$  receptor, found in the peripheral and in the central nervous system (CNS), has been cloned in 1992 [214]. Its modulation may influence numerous physiological conditions including anxiety, diabetes, obesity, or appetite disorders. Most recently, the  $Y_5$  receptor has been cloned and characterized to be involved in food intake regulation [212]. A review published by Ling in 1999 reports on the patent situation related to NPY antagonists [210]. In this contribution representative examples of

potentially active nonpeptide NPY antagonists will be described according to their target receptors.

 **$Y_1$  Receptor Antagonists**

A number of  $Y_1$  antagonists (Fig. (30)) published over the last ten years show binding affinities in the nanomolar range, e.g. as BIBP3226 95 ( $K_i=7.2$  nM), SR120819 96 ( $K_i=15$  nM), PD160170 97 ( $K_i=48$  nM), and LY-357897 98 ( $K_i=0.75$  nM) (Fig. (30)) [215-218]. The best characterized  $Y_1$  antagonist BIBP3226 95 has been demonstrated to inhibit NPY-mediated vasoconstriction and pressure variations [215]. SR120819 96 represents a dipeptide analogue containing a sulfonamide. This orally active antagonist incorporating a central arginine mimic (benzamidine in 96) develops its potency in the 1,4-cis-disubstituted cyclohexyl ring by antagonizing NPY-mediated pressure responses [219].

Parke-Davis discovered a new and unique class of moderately potent but selective  $Y_1$  antagonists by random screening of which PD160170 97 is a representative compound. Eli Lilly described LY-357897 98 from a series of trisubstituted indoles and benzimidazoles. Compound 99 (Fig. (30)) [220] showing a  $K_i$  value of 2.1  $\mu\text{M}$  was discovered by a biased screening of the in-house library and served as lead structure in the subsequent SAR studies of the trisubstituted indole series. Consequent structure modification led to 98, the most active analogue ( $K_i=0.75$  nM), which, in (S)-configuration inhibits NPY-induced forskolin-stimulated cAMP release and intracellular  $\text{Ca}^{2+}$  release in the nanomolar range. The corresponding

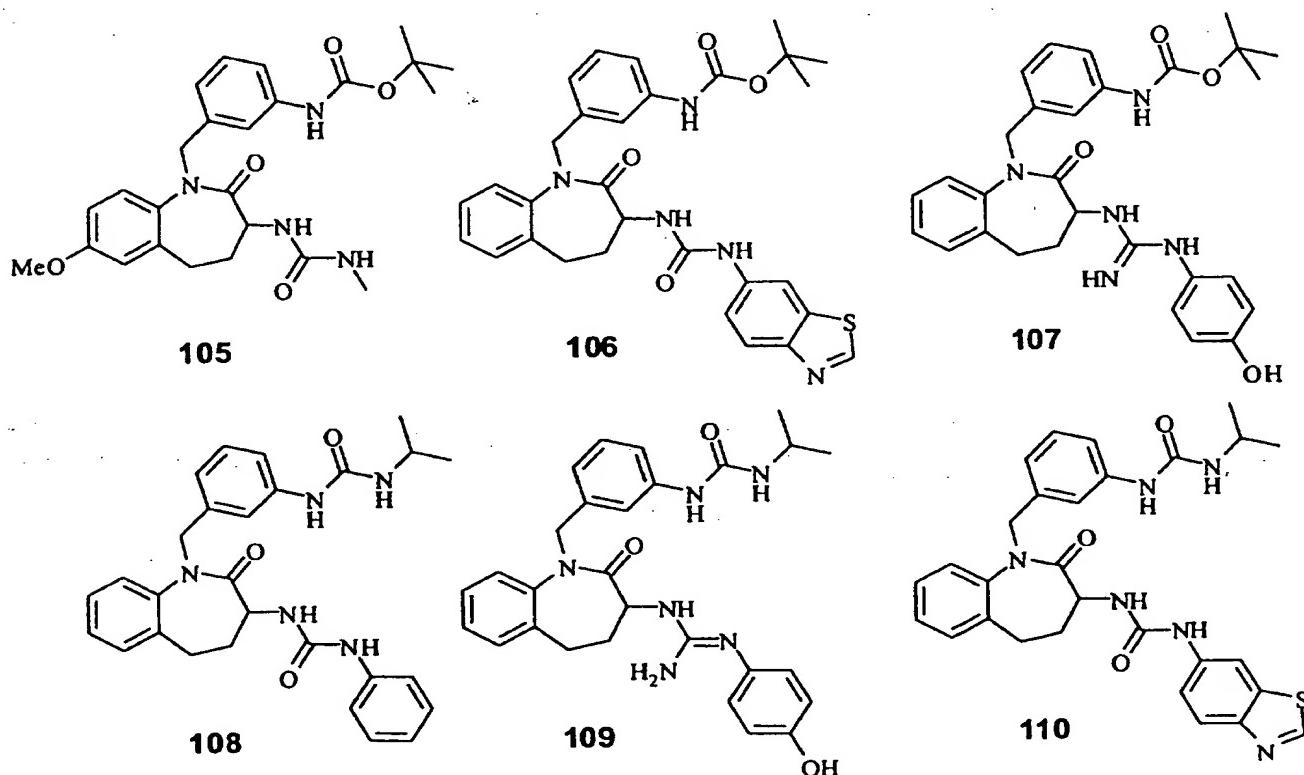


Fig. (31). Benzazepinone-type  $Y_1$  antagonists.

benzimidazole series has also been investigated [221]. A representative example is given by compound 100 (Fig. (30)) which was obtained after systematic optimization of the N1- and C4-substituents of the benzimidazole scaffold. Compound 100 exhibits *in vitro* binding affinity on AV-12 cells expressing the human Y<sub>1</sub> receptor with a K<sub>i</sub> value of 1.7 nM.

Pfizer claimed a series of piperazinyl-comprising compounds as Y<sub>1</sub>-selective antagonists [222]. Analogue 101 (Fig. (30)) demonstrates an interesting activity profile by expressing a differentiated behaviour of the two conformers, i.e. *cis*- (IC<sub>50</sub>=76 nM) and *trans*- (IC<sub>50</sub>=525 nM) exposed ethyl substituent with respect to the phenylpiperazine substituent of the cyclohexyl ring.

Warner Lambert filed compounds based on a quinoline scaffold that were claimed as Y<sub>1</sub> subtype selective antagonists. The 6-aryl-sulfonyl-quinoline analogue 102 (Fig. (30)) inhibits [<sup>125</sup>I]PYY binding to the human Y<sub>1</sub> receptor with an K<sub>i</sub> value of 48 nM [223].

Alanex Corp. claimed two series of compounds containing either an amidino-urea or a diamidino-urea core structure. A representative of the latter series is given by 103 (Fig. (30)) inhibiting the binding of [<sup>125</sup>I]PYY to the Y<sub>1</sub> receptor in membranes derived from human neuroblastoma cell lines (SK-N-MC) with an IC<sub>50</sub> value of 70 nM [224].

Bristol Myers Squibb's patents enclose two structurally related compound classes, i.e. phenyl-dihydropyridines [225] and phenyl-dihydropyrimidines [226]. In compound 104 (Fig. (30)) the *m*-substituted phenyl-dihydropyridine sidechain is terminated with a spiroindane, a structural element which is also found among other antagonists directed against numerous members of the peptide-binding GPCR superfamily.

Murakami *et al.* [227] at Shionogi published a novel class of 1,3-disubstituted benzazepinones as potent and selective Y<sub>1</sub> antagonists. Based on the lead compound 105

(Fig. (31)) (K<sub>i</sub>=1.5 μM) which emerged from a random screening approach, follow-up compounds 106 (K<sub>i</sub>=160 nM) and 107 (K<sub>i</sub>=39 nM) have been obtained (Fig. (31)).

Further optimization of the phenyl substituent in position 3 leading to analogue 108 as well as optimization of the substituent in position 3 of the 2,3,4,5-tetrahydro-1*H*-1-benzazepin-2-one, represented by congener 109 (Fig. (31)) resulted in an increase of the binding affinity towards 43 nM and 2.9 nM, respectively. Combination of the optimized structural features led to one of the most potent derivatives (110, Fig. (31)) which competitively inhibits specific [<sup>125</sup>I]PYY binding to Y<sub>1</sub> receptors in human SK-N-MC cells with a K<sub>i</sub> value of 5.1 nM. Although 110 also antagonizes the Y<sub>1</sub> receptor-mediated increase in cytosolic free Ca<sup>2+</sup> concentration in SK-N-MC cells, it has not been evaluated *in vivo* because of its poor solubility in aqueous solution and poor oral bioavailability. Hence, it has been shown in binding assays with 17 receptors including the Y<sub>2</sub>, Y<sub>4</sub>, and Y<sub>5</sub> receptor that it binds selectively to the Y<sub>1</sub> receptor [227].

#### Y<sub>5</sub> Receptor Antagonist

Several patent applications have been filed by Novartis in 1997 [228-230] claiming diamino quinazolines as selective Y<sub>5</sub> antagonists. They were shown to inhibit NPY-induced Ca<sup>2+</sup> increase in stable transfected cells expressing the Y<sub>5</sub> receptor. Analogue 111 (Fig. (32)) decreases food intake by 60% in 24 h food deprived rats after *i.p.* administration of 30 mg/kg.

In 1998 Banyu Pharm. [231,232] and Bayer [233] filed patents including aminopyrazoles, aminopyridines and an amide based core structure as Y<sub>5</sub> antagonists. The Banyu compounds 112 and 113 showed IC<sub>50</sub> values for Y<sub>5</sub> binding of 8.3 nM and 4.1 nM, respectively [234], whereas the Bayer compound 114 binds with an IC<sub>50</sub> value of 0.47 nM. Also this congener shows selective affinity for the Y<sub>5</sub> receptor compared to Y<sub>1</sub>, Y<sub>2</sub>, or Y<sub>4</sub> receptor subtypes (Fig. (32)) [234].

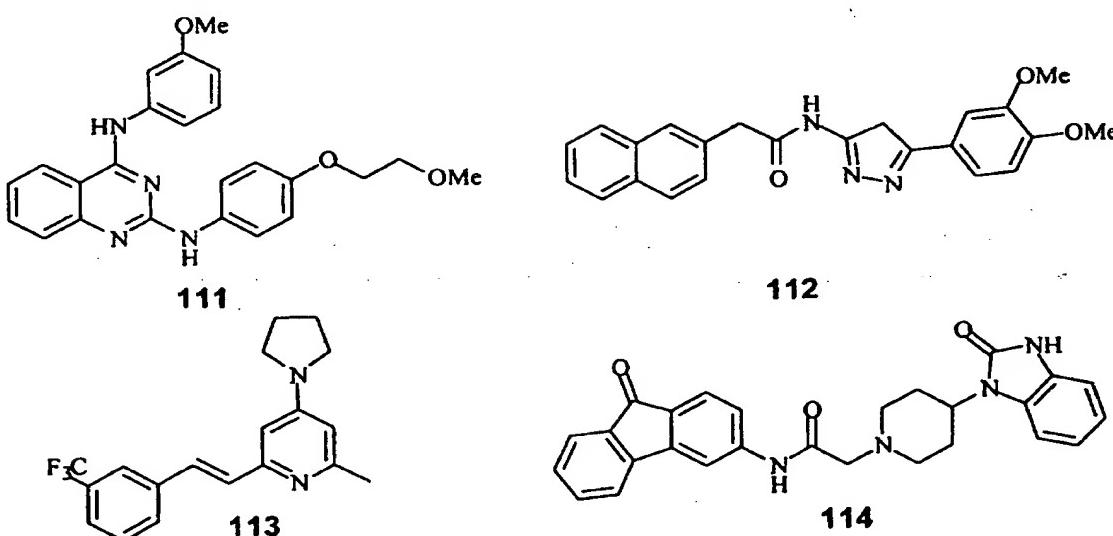


Fig. (32). Y<sub>5</sub> antagonists.

## STRUCTURAL-BASED DRUG DESIGN

After having addressed the classical lead finding approach characterized by screening compound libraries with subsequent optimization, the complementary strategy of structure-based design will be highlighted, since this strategy is about to change the classical paradigm of "random versus rational" in favour of "random goes rational". Due to the fact that no high-resolution structure of any GPCR protein is available, all design attempts are still restricted on comparative analyses of structural features of biologically characterized low-molecular weight compounds which are interpreted in terms of steric and physicochemical complementarity to a hypothetical receptor binding site. Currently pursued GPCR research projects represent textbook examples for the fruitful combination of ligand-derived rationales that are incorporated into e.g. the design of combinatorial chemistry programs with the aim to direct resulting libraries more efficiently to the target class of interest, rather than attempting to explore systematically the infinite universe of molecular diversity. In the following, a few representative research efforts will be introduced that clearly attempt to change the mainstream of classical lead finding programs in favour of knowledge-based approaches.

## Somatostatin

Somatostatin (Somatotropin Release-Inhibiting Factor, SRIF) (Table 1) was discovered because of its inhibitory effect on growth hormone secretion. The peptide hormone which exists in two biologically active forms, the 14 amino acid form (SRIF-14) and the 28 amino acid form (SRIF-28), acts as a neuromodulator [235].

Five receptor subtypes for somatostatin ( $sst_1$ - $sst_5$ ) have been cloned and characterized from human tissue [236]. Apart from its pivotal role as neuromodulator within the central nervous system (CNS), somatostatin alters the secretion of growth hormone (GH), insulin, glucagon, pancreatic enzymes, and gastric acid [237-240]. Consequently, analogues of somatostatin emerged as interesting tools in the treatment of disorders linked to the above mentioned physiological functions. Somatostatin agonists may therefore be used for the treatment of acromegaly, diabetes, cancer, rheumatoid arthritis, and Alzheimer's disease. Especially  $sst_2$ -selective agonists emerged as useful candidates for the treatment of acromegaly, retinopathy, and diabetes [241,242].

The area of somatostatin agonist and antagonist research is a textbook example for indirect drug design utilizing ligand-derived structural rationales for design purposes. In the beginning of the 1990's numerous design projects were pursued aimed to replace the peptide scaffold of the pharmacophoric portion of somatostatin (SRIF-14) yielding a variety of moderately active, chemically diverse compounds. More recent lead finding programs employ the highly efficient technology of combinatorial chemistry for rapid modification of promising hits culminating in subtype-selective high-affinity binding compounds from a series of designed libraries. A brief overview of both, the rational design of single somatostatin-based peptidomimetics as well as the combinatorial chemistry-based approaches for lead identification and optimization will be given after a short description of the somatostatin-relevant pharmacophore hypothesis.

The tetradecapeptide SRIF-14 115 (Fig. (33)), one of the widely distributed active forms of somatostatin, is believed

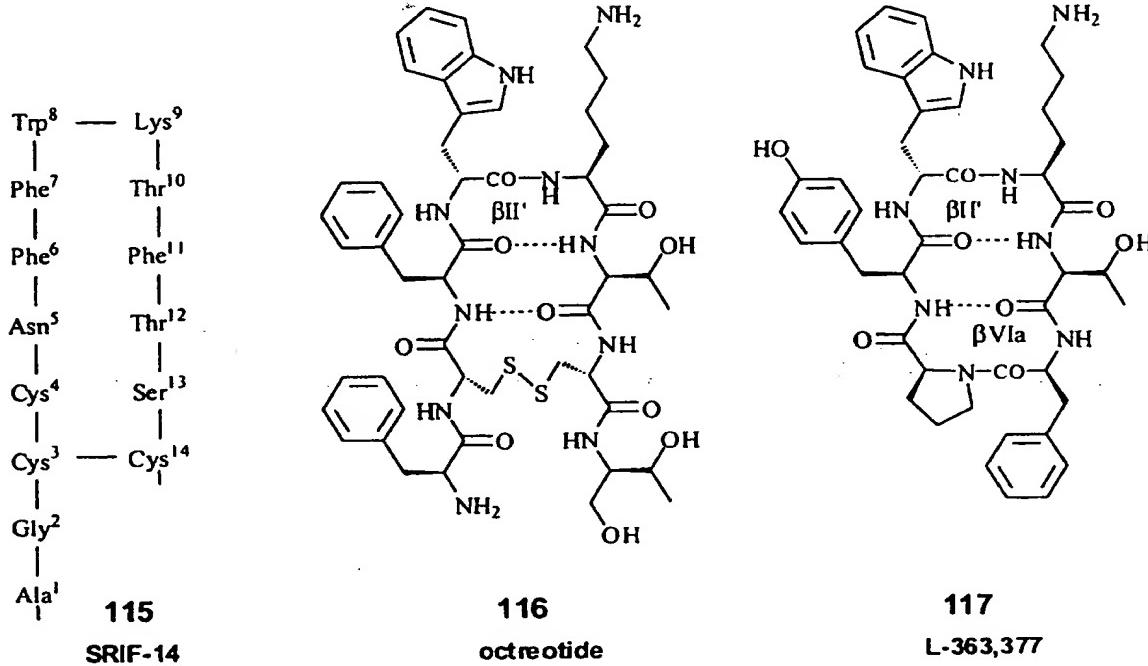
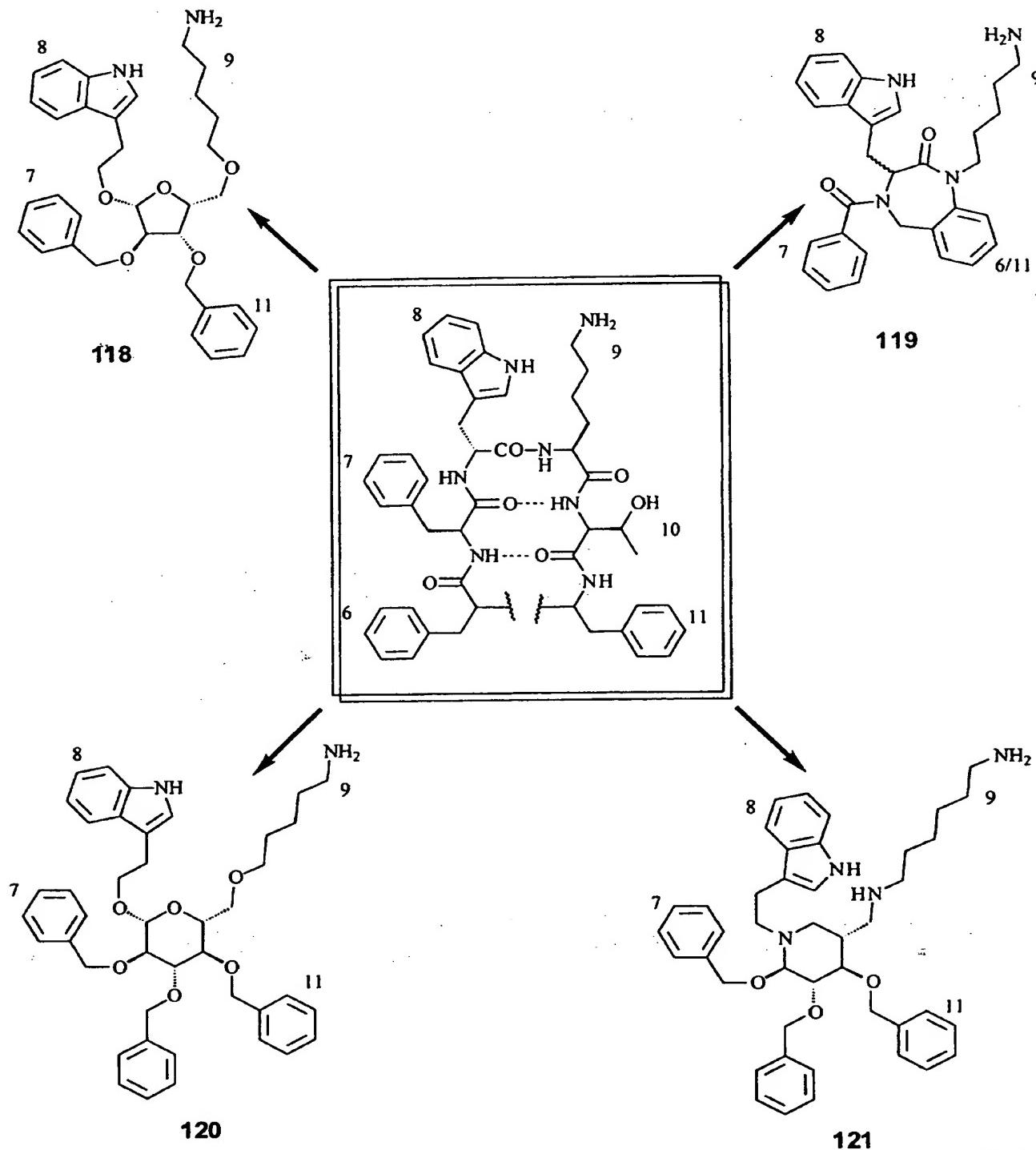


Fig. (33). Conformational preferences of somatostatin-derived peptide analogues.

to adopt a two-stranded  $\beta$  sheet conformation induced by a  $\beta$  turn encompassing Phe<sup>7</sup>-Trp<sup>8</sup>-Lys<sup>9</sup>-Thr<sup>10</sup>, and the disulfide bridge between Cys<sup>3</sup> and Cys<sup>14</sup>, respectively (Fig. (33)). The conformation is further stabilized by the transannular H-bonding pattern typical for antiparallel sheet structures. From

numerous sequence- and structure-activity studies it turned out that the primary pharmacophore consists of the  $\beta$  turn forming residues Phe<sup>7</sup>-Trp<sup>8</sup>-Lys<sup>9</sup> and an additional lipophilic binding element reminiscent to Phe<sup>6</sup>/Phe<sup>11</sup> [243].



**Fig. (34).** Peptide conformation-derived non-peptide somatostatin antagonists. The numbering scheme refers to that of SRIF-14 (see Fig. (33)).

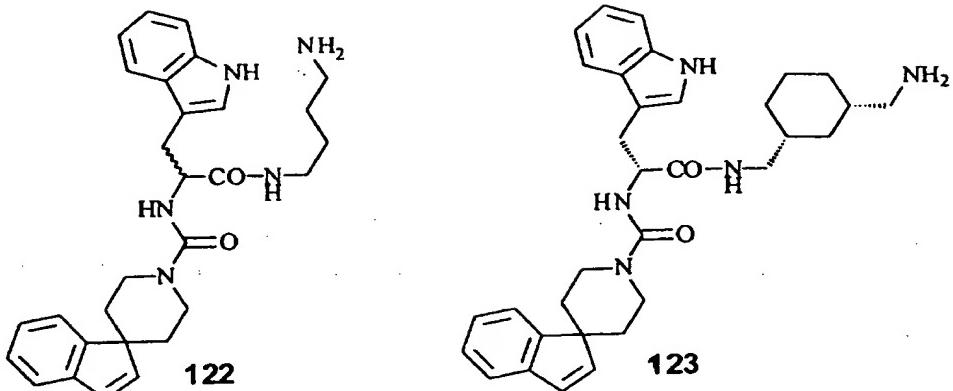


Fig. (35). High-affinity *hss2* antagonists derived by screening and subsequent optimization.

The experimentally derived conformations of the metabolically more stable peptide analogues, e.g. octreotide (Sandostatin®) 116 [244,245] or L-363,377 117 [246,247] not only prove the pharmacophore hypothesis, but were further used as template structures underlying a series of rational design attempts (Fig. (33)). In 1992, researchers at Sandoz designed a tetra-substituted xylofuranose derivative 118 (Fig. (34)) positioning the sidechains of Phe<sup>7</sup>-Trp<sup>8</sup>-Lys<sup>9</sup> at its C-2, C-3, and C-5 atoms, while the benzyloxy group attached to C-3 resembles the aromatic sidechain of Phe<sup>11</sup>, respectively (Fig. (34)) [248].

The xylose derivative 118 displaced radio-labelled octreotide 116 from its receptor with an IC<sub>50</sub> of 23 μM.

Even though the mutual steric fit of the xylose-based mimic and the somatostatin structure was reasonable, the compounds displayed only moderate affinity which was attributed to the loss of considerable conformational entropy during receptor binding. Consequently, the design strategy at Sandoz was directed towards more rigid compounds based on nonpeptide scaffolds. For the purpose of substituting the peptide backbone of SRIF-14 within the β turn portion the privileged structure of the 1,4-benzodiazepinone was employed from which the pharmacophoric groups could radiate into the periphery [249]. The resulting nonpeptide tetrapeptide-mimetic 119 (Fig. (34)) was designed to account for the sidechains of Phe<sup>7</sup>-Trp<sup>8</sup>-Lys<sup>9</sup> by the appropriate substituents, while the aromatic ring of the benzodiazepine

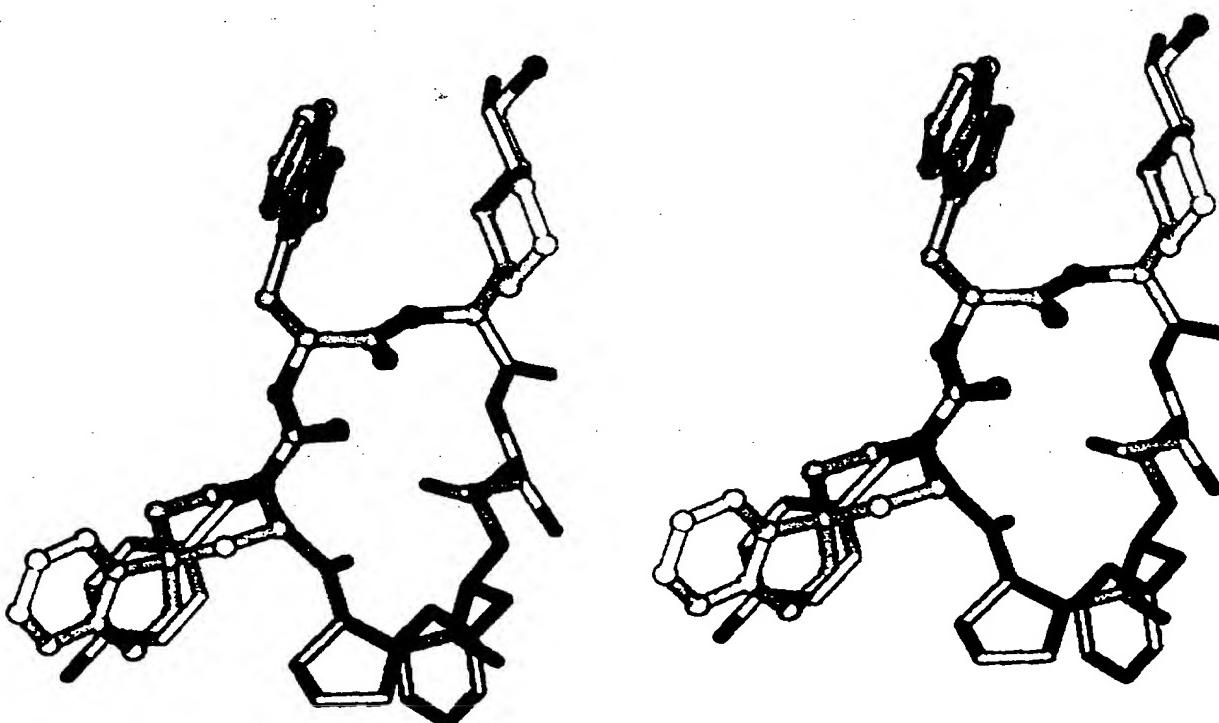


Fig. (36). Side-by-side stereo presentation of the structural overlay of 123 (ball-and-stick mode) onto the experimentally-derived conformation of 117 (stick-mode).

core was believed to mimic the additional lipophilic element referring to Phe<sup>6</sup>/Phe<sup>11</sup>, respectively. However, the racemic mixture of 119 (benzodiazepinone) showed an IC<sub>50</sub> of 7 μM, and even after separation, the L- and D-Trp containing benzodiazepinone displaced the radioligand with IC<sub>50</sub> of only 6.5 μM and 8.2 μM, respectively.

Similar affinities in the low micromolar range were obtained with peptidomimetics based on β-D-glucose scaffolding described by Hirschmann and Nicolaou at the end of the 80's and beginning of the 90's [250]. Molecular modeling studies carried out on the 3D structures of SRIF-

14 115 and analogues of L-363,377 117 suggested that substituents at C-2, C-1, and C-6 of a β-D-glucose template resemble the orientational pattern of the β turn-forming amino acids of the somatostatin-derived peptides. The corresponding penta-substituted glucose 120 (Fig. (34)) showed an IC<sub>50</sub> of 15 μM.

In 1996, researchers from Rhône-Poulenc Rorer published a similar approach of *de-novo* designed peptidomimetics employing aza-sugar-based templates for the spatially controlled orientation of the pharmacophoric amino acid sidechains [251]. Independent of ring size and substitution

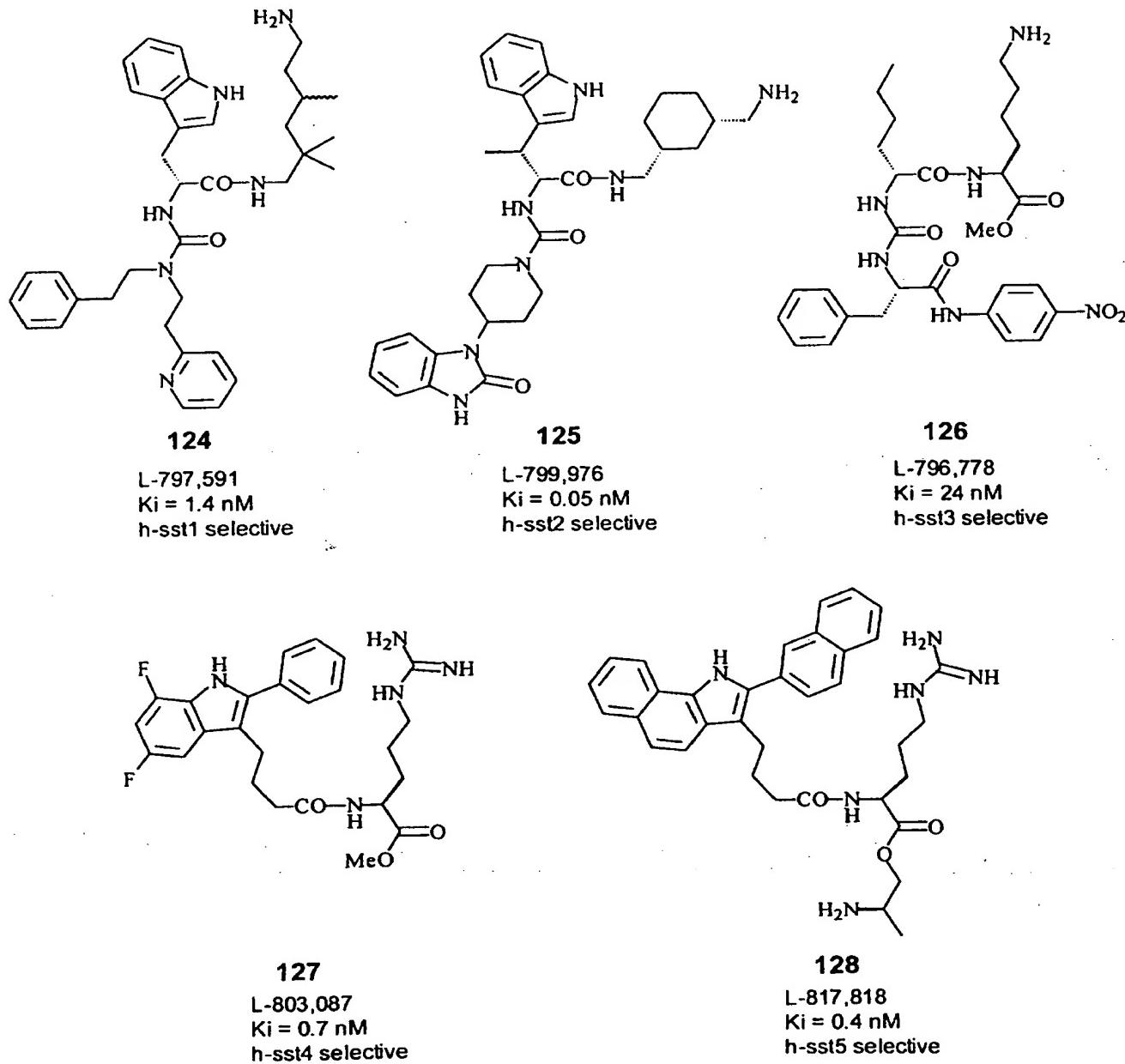


Fig. (37). For each somatostatin receptor subtype (*hsst1*-*hsst5*) highly selective compounds emerged from rationally designed combinatorial libraries.

pattern, all analogues showed weak affinity with  $IC_{50}$  values in the range of 10–15  $\mu\text{M}$  (see for example 121, Fig. (34)).

Over the last two years, scientists at the Merck Research Laboratories conducted a comprehensive program aimed to identify subtype-selective peptidomimetic compounds for each somatostatin receptor subtype ( $\text{sst}_1$ - $\text{sst}_5$ ) by following a rational design strategy using a combination of classical medicinal chemistry with modern combinatorial chemistry techniques [252–256]. The primary lead, L-264,930 122 (Fig. (35)), that initiated that combined approach, was identified by a virtual screening of the Merck sample collection. The 3D structure of the cyclic hexapeptide L-363,377 117 (Fig. (33)) served as spatial probe in that a geometric pattern, describing the arrangement of the pharmacophoric groups, was derived by means of molecular modeling. After similarity searches, in which the sidechains of residues  $\text{Tyr}^7$ - $\text{Trp}^8$ - $\text{Lys}^9$  were given priority for the pharmacophore definition, L-264,930 122 was uncovered with submicromolar affinity for the  $hsst_2$  receptor.

This compound became the primary focus for medicinal chemistry and combinatorial chemistry at Merck. By constraining the floppy diamine chain with a 1,3-bis-aminomethyl-cyclohexane moiety the compound was optimized to yield L-054,264 123 (Fig. (35), Fig. (36)) with an  $IC_{50}$  of 1.6 nM for the  $hsst_2$  receptor and a more than 1000-fold selectivity over all other somatostatin receptor subtypes.

Simultaneously, L-264,930 122 served as lead structure for a targeted combinatorial library. For library design the lead was dissected into three components, notably the central  $\alpha$ -amino acid, the C-terminal blocking diamine, and the N-terminal blocking bulky urea-attached amine. The initial library was based on 20  $\alpha$ -amino acids, that were mainly analogues of Trp or carried modified aromatic sidechains. Additionally, 20 diamines were chosen in which the spacing between the two nitrogens varies between four and six atoms, also encompassing different ring topologies. The amine collection comprised 79 different entities that were

biased towards piperidines and piperazines containing additional aromatic rings, so-called "privileged structures". A solid-phase mix-and-split protocol was used to synthesize more than 130000 compounds in complex mixtures that demanded a deconvolution strategy. After several rounds of iterative optimization employing classical analoging as well as follow-up libraries, five compounds 124 – 128 emerged with the desired activity and selectivity profile, in that each compound is highly selective for a distinct somatostatin receptor subtype (Fig. (37)).

This program impressively demonstrates the impact of an intelligent combination of structural rationales derived by comprehensive molecular modeling with the synthetic efficiency of current combinatorial chemistry techniques for lead finding attempts within modern medicinal chemistry.

A further example of a peptidomimetics-based library employing structure rationales for identification of subtype-selective somatostatin analogues was published recently by J. Ellman and co-workers (Fig. (38)) [257]. By decoration of a medium-sized heterocyclic  $\beta$  turn mimic with the Trp- and Lys-sidechain in positions  $i+1$ - $i+2$  and vice versa, together with an additional amine building block in  $i+3$ , a remarkably small library of only 172 entities (22 amines, D/L-Trp-D/L-Lys, D/L-Lys-D/L-Trp) uncovered a  $hsst_5$ -selective compound 129 with an  $IC_{50}$  of 87 nM.

### Bradykinin

Researchers at Sterling Winthrop considered angiotensin-converting-enzyme (ACE) inhibitors as templates for the design of BK  $B_2$  receptor antagonists [258], since ACE degrades both, angiotensin II (All) and BK by cleaving the Pro $^7$ -Phe $^8$  amide bond. Therefore, an ACE inhibitor was considered to display properties or conformational similarities to BK, thus establishing a pharmacophoric link between ACE and BK receptors in that both macromolecules recognize similar steric and physicochemical features. In order to test this hypothesis, the ACE inhibitor Quinapril

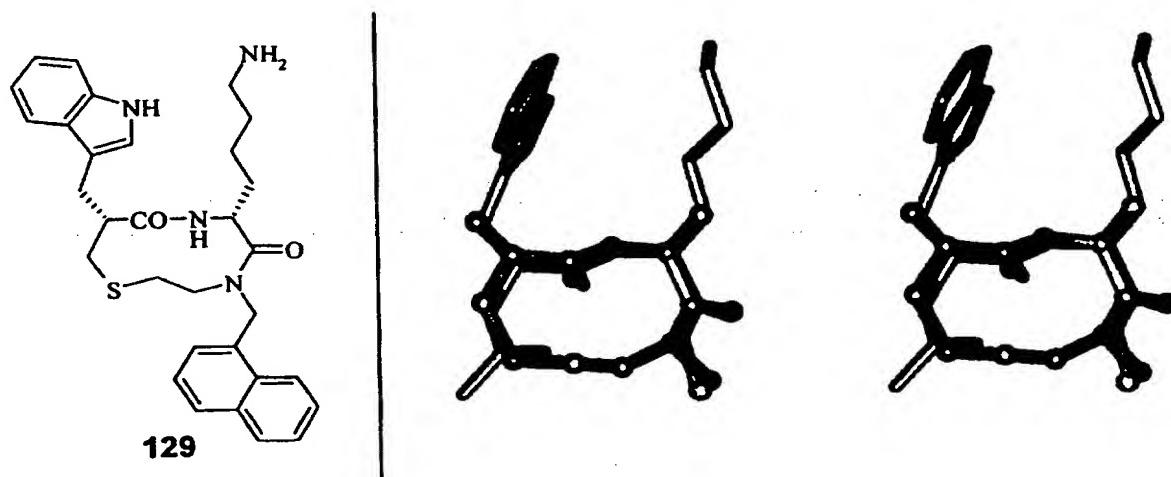


Fig. (38). Left:  $hsst_5$ -selective compound derived from a  $\beta$  turn-templated library; right: side-by-side stereo presentation of the structural superposition of the  $\beta$  turn mimic (ball-and-stick mode) onto the  $\beta$ II' turn portion of 117 (stick-mode).

130 (Fig. (39)) [259] was chosen as template for the design and synthesis of a series of *homo*Phe-Tic (Tic: tetrahydriisoquinoline) containing compounds. The diastereomeres of 131 (Fig. (39)) exhibit binding affinities in the micromolar range ( $K_i = 1 \mu\text{M}$ ) in [ $^3\text{H}$ ]BK binding studies with human IMR-90 fetal lung fibroblasts.

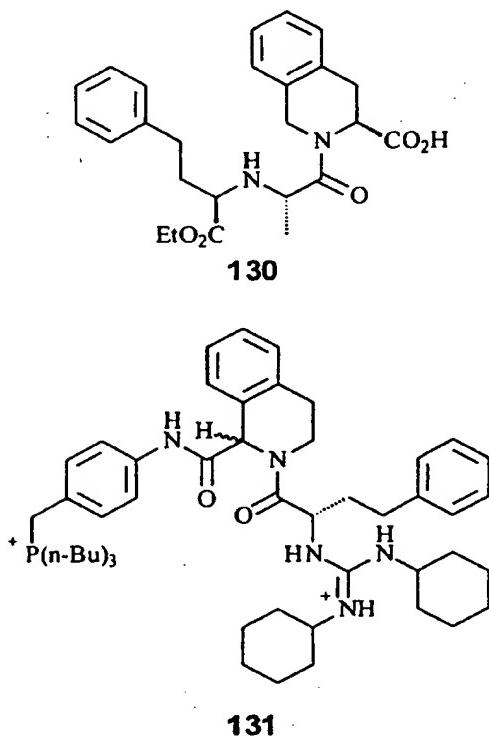


Fig. (39). Quinapril (130) served as template for the design of BK antagonists (e.g. 131).

Goodfellow *et al.* [260] followed a different approach in that they established a library based on a  $\beta$  turn template, CP-0597 132 (Fig. (40)) [261] which is a peptidic  $B_1/B_2$  antagonist containing D-Tic and N-Chg (Chg: N-cyclohexylglycine) in  $i+1$  and  $i+2$  position of a  $\beta$ II' turn. Starting from that structural rationale, the peptidomimetic

CP-2055 133 (Fig. (40)) was generated. Based on the 1,4-piperazine scaffold a combinatorial library has been designed to produce approximately 2500 *rationally directed diverse analogues* (RDDA), 134 (Fig. (40)).

This process led to the discovery of nonpeptide  $B_2$  antagonists serving as lead compounds for traditional optimization. While the parent peptidic analogue CP-0597 132 shows an  $\text{IC}_{50}$  value of 0.33 nM, CP-2055 133 exhibits an  $\text{IC}_{50}$  value of about 55  $\mu\text{M}$  on a cloned human  $B_2$  receptor. CP-2458 is a further a member of the designed library 134 and inhibits human  $B_2$  receptor binding ( $\text{IC}_{50}=4.1 \mu\text{M}$ ) and BK-stimulated  $\text{Ca}^{2+}$  flux in human fibroblasts ( $\text{IC}_{50}=19 \mu\text{M}$ ). Unfortunately, the chemical formula of the compound is not given explicitly in the publication.

Based on two structural templates (i) a cyclic hexapeptide BK antagonist 135 [262] and (ii) the nonpeptide BK antagonist WIN-64338 43 (Fig. (41)) [129], Dankwardt *et al.* [263] designed nonpeptide  $B_2$  antagonists. While the hexapeptide served as structural template for the positioning of relevant functionality, WIN-64338 43 served as rigid scaffold for the design of a series of naphthylalanine containing derivatives, none of which showed improved affinity for the  $B_2$  receptor when compared to WIN-64338 43 ( $K_d = 44 \text{ nM}$ ). Substitution of the phosphonium group against the corresponding ammonium moiety resulted in a two-fold decrease in affinity for the  $B_2$  receptor. However, the proposed structural superposition of the cyclic hexapeptide 135 with the blocked amino acid derivative 43 provided a pharmacophore hypothesis that enabled Dankwardt and coworkers to design moderately active compounds and might serve as structural blueprint for further design attempts[263].

#### Neurokinin

The structural feature of a reverse  $\beta$  turn has emerged to a general design principle underlying a variety of GPCR antagonist projects.  $\beta$  turns play an important role in recognition phenomena as documented e.g. for somatostatin and NKA which bind to their receptors in a proposed  $\beta$  turn conformation. Therefore Horwell *et al.* [264] at Parke-Davis

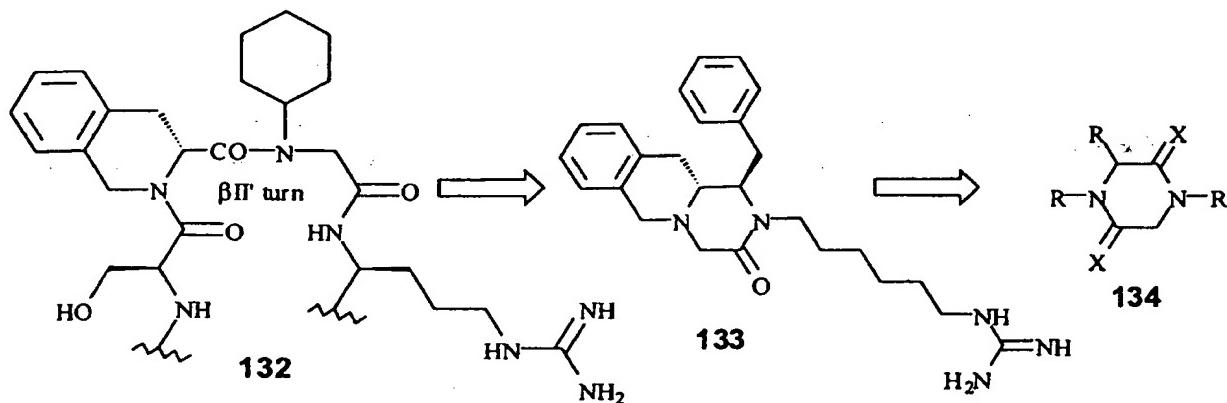


Fig. (40). Design strategy of BK antagonists following the "rationally directed diverse analogues" approach.

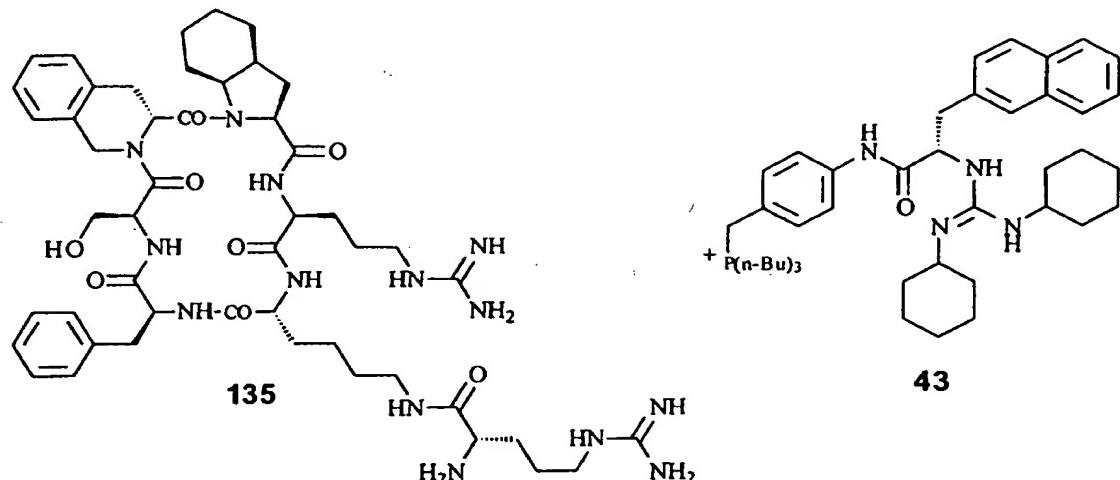


Fig. (41). Rationally designed BK antagonists.

decided to employ  $\beta$  turn mimetics for the design of compounds with affinity for the NK<sub>2</sub> receptor. Starting from the x-ray structure of MEN-10627 136 (Fig. (42)) [265], a cyclic hexapeptide displaying high NK<sub>2</sub> affinity, a pyrrolidine-based Trp-Phe dipeptide mimetic 137 has been designed (Fig. (42)).

The Trp-Phe dipeptide scaffold mimics the Trp-Phe fragment in the central portion ( $i+1$ ,  $i+2$ ) of a  $\beta$ I turn within the cyclic hexapeptide which folds into a  $\beta$ I/ $\beta$ II turn conformation. Although the indole and benzyl sidechains of both compounds superimpose satisfactorily, 137 did not show significant NK<sub>2</sub> receptor affinity. The lack of affinity has been attributed to the misfit of the dipole moments of both molecules. In order to address this problem in more detail, a further Trp-Phe dipeptide mimetic 138 (Fig. (42)) has been designed by computer-assisted molecular modeling identifying a 2-azabicyclonorbornan spacer to be more favourable compared to the pyrrolidine (Fig. (43)).

Comparison of the binding affinities revealed that the conversion of the hexapeptide to a dipeptide unit results in the loss of high binding affinity (MEN-10627 136:  $IC_{50}=0.079$  nM (NK<sub>2</sub>); 137:  $IC_{50}=14\%$  @ 10  $\mu$ M (NK<sub>2</sub>); 138:  $IC_{50}=31\%$  @ 10  $\mu$ M (NK<sub>2</sub>)) studied by displacement assays with [<sup>125</sup>I]NKA in hamster urinary bladder. On the other hand, [<sup>125</sup>I]BH-SP displacement from NK<sub>1</sub> in human IM-9 cells of MEN-10627 136 ( $IC_{50}=0.8$   $\mu$ M) is retained by 137 and 138 with  $IC_{50}$  values of 3.7  $\mu$ M and 6.7  $\mu$ M, respectively. Interestingly, the dipeptide mimetics exhibit some binding affinity to human NK<sub>3</sub> receptors stably expressed in CHO cells shown by replacement of [<sup>125</sup>I]-[MePhe<sup>7</sup>]NKB (137:  $IC_{50}(NK_3)=3.5$   $\mu$ M; 138:  $IC_{50}(NK_3)=35\%$  @ 10  $\mu$ M) while the parent hexapeptide exhibited no NK<sub>3</sub> affinity at all.

Only recently, Porcelli *et al.* [266] presented the design of a SP antagonist based on a cyclic pentapeptide with the chirality sequence following a D<sup>1</sup>L<sup>2</sup>D<sup>3</sup>D<sup>4</sup>L<sup>5</sup> pattern. The

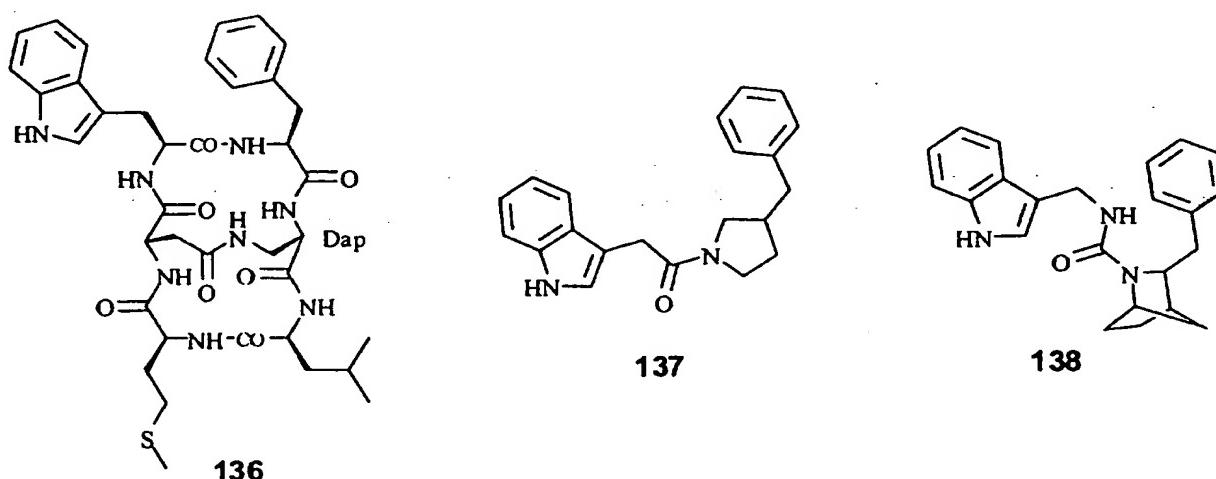


Fig. (42). Peptide structure-derived rationales were used to design non-peptide NK antagonists (Dap: 2,3-diaminopropanoic acid).

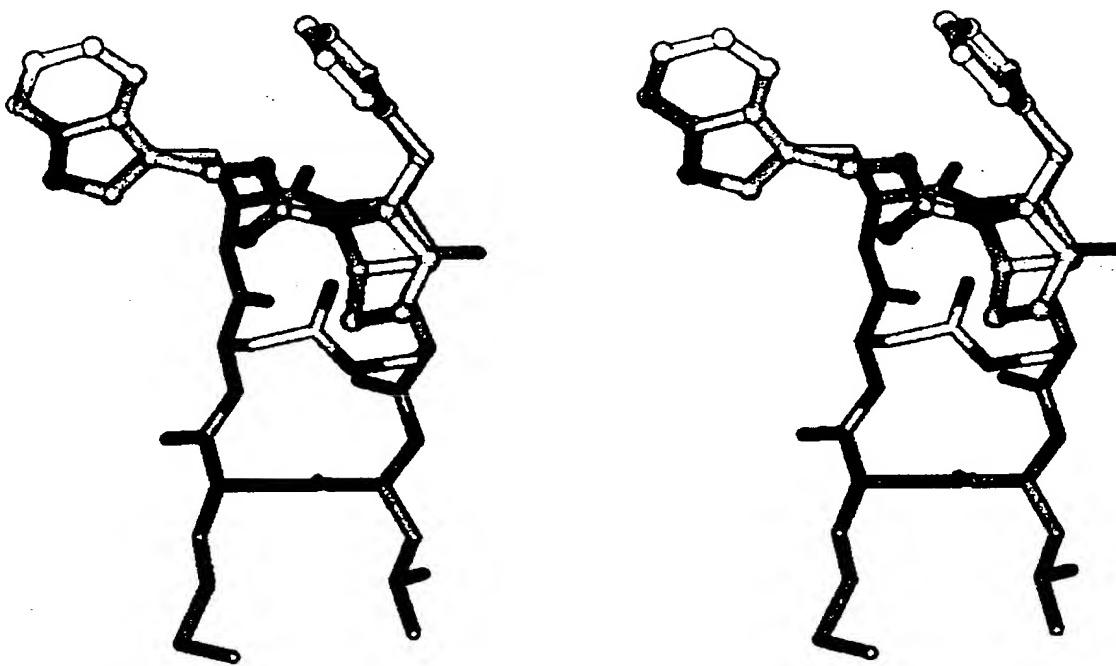


Fig. (43). Side-by-side stereo presentation of the structural overlay of 138 (ball-and-stick-mode) onto the x-ray structure of 136 (stick-mode) within the turn corresponding portion.

authors suggest this scaffold as a generic template to design antagonists also for other members of the GPCR family. This suggestion is the logical consequence of the fact that among potent GPCR antagonists the same unique skeleton is found among other representatives of antagonists for peptide-binding GPCRs, e.g. the natural pentapeptide BE-18257B (*cyclo*-(D-allo-Ile-Leu-D-Trp-D-Glu-Ala-)) and its synthetic analogue BQ-123 (*cyclo*-(D-Val-Leu-D-Trp-D-Asp-Pro-)) [267], a prominent ET<sub>A</sub> antagonist. Both cyclic pentapeptides follow the chiral sequence pattern of DLDDL. The solution structure of BQ-123 [268] exhibits a typical  $\beta$ II/ $\gamma$  turn arrangement characteristic for this class of molecules. Based on the same structural template, Porcelli *et al.* designed a SP antagonist, ITF-1565 (*cyclo*-(D-Trp<sup>1</sup>-Pro<sup>2</sup>-D-Lys<sup>3</sup>-D-Trp<sup>4</sup>-Phe<sup>5</sup>)) which inhibits NK<sub>1</sub>-mediated SP-induced contraction of the rabbit caval vein. ITF-1565 only shows modest NK<sub>2</sub> activity and was inactive in ET<sub>A</sub> assays. ITF-1565 exhibits a  $\beta$ II/ $\gamma$  turn arrangement with Pro<sup>2</sup> in *i*+1 and D-Lys<sup>3</sup> in *i*+2 position of the  $\beta$  turn and Phe<sup>5</sup> in the

central position of the  $\gamma$  turn. Interestingly, the authors succeeded to superimpose the sidechain functionalities of D-Trp<sup>4</sup>, Phe<sup>5</sup> and D-Trp<sup>1</sup> within ITF-1565 well onto the indole and benzyl rings within a  $\beta$ -D-glucose derived SP antagonist 139 (Fig. (44)).

#### Luteinizing Hormone-Releasing Hormone

The decapeptide amide Luteinizing Hormone-Releasing Hormone (LHRH, Table 1) [269], *p*Glu-His-Trp-Ser-Tyr-Gly-Leu-Arg-Pro-Gly-NH<sub>2</sub>, is released from the hypothalamus and stimulates the anterior pituitary gland resulting in the secretion of the gonadotropins luteinizing hormone (LH) and follicle-stimulating hormone (FSH). LHRH, also termed gonadotropin-releasing hormone, plays an important role in the regulation of reproductive functions, thus rendering its synthetic analogues useful tools for the treatment of endocrine-based diseases like prostate and breast cancer, endometriosis, uterine leiomyoma, and precocious puberty [270]. Even though LHRH agonists proved to be useful in the treatment of the above mentioned diseases [271-273], research has also focused on the development of potent and safe antagonists.

Recently, Takeda presented a substituted 4-oxothieno[2,3-*b*]pyridine as a highly potent and orally active nonpeptide antagonist of the human LHRH receptor [274]. Again, this research program was based on the structural characteristics of a  $\beta$  turn suggested as the dominant conformational feature within [5-8]LHRH (Fig. (45)) [272,273].

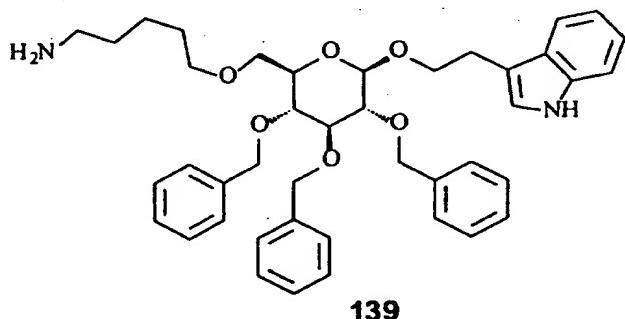


Fig. (44). Glucose-based peptidomimetic NK analogue.

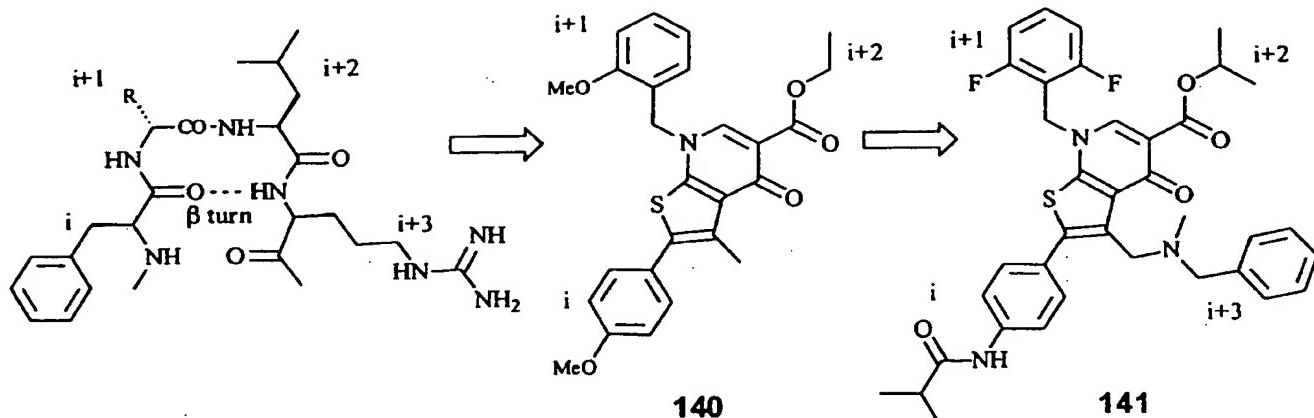


Fig. (45).  $\beta$  turn-derived design strategy uncovered highly active non-peptide LHRH analogues.

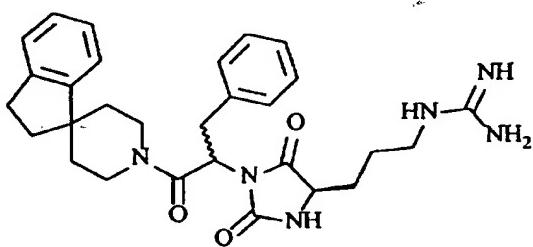
The  $\beta$  turn is considered to represent the bioactive conformation of LHRH in the receptor-bound state. Therefore, the structural element of a  $\beta$  turn was attempted to be transferred onto a rigid scaffold which mimics the  $\beta$  turn and can be decorated with the crucial functionalities, thus positioning them into the receptor-complementary orientation (Fig. (45)). For this purpose, a directed screening approach was initiated aimed to uncover compounds showing similarity to the turn template. The screening towards the inhibitory effect on the specific binding of [ $^{125}$ I]leuprolelin to human LHRH receptor [275] expressed in CHO cells resulted in the initial lead compound 140 (Fig. (45)) [274].

This compound was structurally compared to the hypothesized  $\beta$  turn arrangement and changed in order to fulfil the structural requirement imposed by that template,

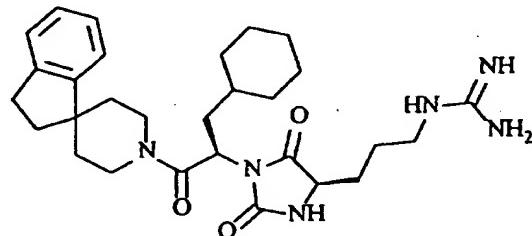
e.g. substituting Gly by hydrophobic D-amino acids increased activity presumably due to stabilization of the  $\beta$  turn by introducing a D-amino acid into the  $i+1$  position of the  $\beta$  turn. Subsequent modifications finally led to the discovery of T-98475 141 (Fig. (45)) exhibiting an  $IC_{50}$  value of 0.2 nM for the binding to the cloned human LHRH receptor. Further, T-98475 141 shows inhibitory effects on LHRH-stimulated LH release in functional *in vitro* and *in vivo* assays. Thus, T-98475 141 is a good candidate of a new class of therapeutics for the treatment of LH-induced dysfunctions in sex-hormone-dependent pathologies.

### C5a

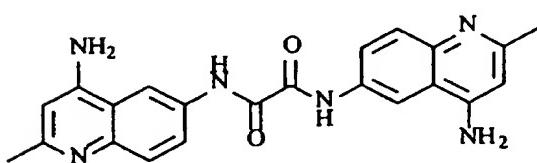
The 74 amino acid peptide C5a (Table 1) is released after activation of the complement system at sites of inflammation



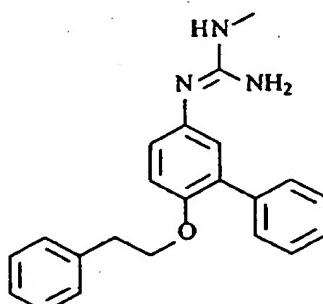
142



143



144



145

Fig. (46). C5a analogues.

by proteolytic cleavage of the complement factor C5 [276]. The hormone-like peptide anaphylatoxin, C5a, acts as chemotaxin by attracting and promoting the degranulation of granulocytes and macrophages during immune response [277,278]. Inappropriate activation of C5a results in a number of inflammatory diseases including rheumatoid arthritis [279], Alzheimer's disease [280], ischemic heart failure [281], psoriasis [282], atherosclerosis [283], and adult respiratory distress syndrome (ARDS) [284]. In this sense, agents preventing the interaction of C5a and its receptor, C5aR, would be useful for inhibition of the pro-inflammatory function of C5a, thus, being a useful therapeutic in the treatment of chronic inflammatory disorders induced by activation of the complement system and the release of C5a [285,286]. The binding of the small protein C5a to its receptor is characterized by two interaction sites. A two-site model has been proposed localizing the major binding epitope for the ligand C5a in the extracellular N-terminal region of the receptor, while the second binding cavity is located in the core of the transmembrane helix bundle, obviously serving as the "activating binding site" recognizing the C-terminal octapeptide of the ligand [287,288]. Starting from the sequence of the native ligand a number of peptide-based antagonists were discovered which have been reviewed only recently by Wong *et al.* [289]. Obviously, the development of a nonpeptide antagonist in this field is a major challenge since research revealed only low molecular weight compounds acting as C5a agonists or at least partial agonists over the last two decades.

Merck identified an initial lead 142 (Fig. (46)) by screening an in-house sample collection for the displacement of [<sup>125</sup>I]C5a from human neutrophil membrane preparations which served for further optimization [290].

The spiroindane-bearing hydantoin 142 has been modified by introduction of a cyclohexylmethyl group instead of the benzyl residue resulting in compound 143 (Fig. (46)) which exhibits an IC<sub>50</sub> value of 0.3 μM.

Surprisingly, functional receptor assays revealed that all compounds of this series with affinity for C5aR showed an agonistic potential. The only nonpeptide antagonists have been reported by Merck investigating 4,6-diaminoquinolines (144) [291] and Rhône-Poulenc Rorer identifying a phenylguanidin by random screening (145, IC<sub>50</sub>=0.8 μM) (Fig. (46)) [292].

As random screening techniques have not brought the expected success, rational design would offer an alternative in the lead finding process for C5a antagonists. Based on the results of conformational studies of cyclic pentapeptide ET antagonists, BE-18257B and BQ-123 [293,294], Wong and co-workers [295,296] followed the same strategy as presented by Porcelli *et al.* [266] for the design of the SP antagonist, ITF-1565. BQ-123, *cyclo*-(D-V<sup>1</sup>-Leu<sup>2</sup>-D-Trp<sup>3</sup>-D-Asp<sup>4</sup>-Pro<sup>5</sup>-) and ITF-1565, *cyclo*-(D-Trp<sup>1</sup>-Pro<sup>2</sup>-D-Lys<sup>3</sup>-D-Trp<sup>4</sup>-Phe<sup>5</sup>-) follow an identical chirality pattern of D<sup>1</sup>L<sup>2</sup>D<sup>3</sup>D<sup>4</sup>L<sup>5</sup> leading to a βII/γ<sub>(i)</sub> turn arrangement with L<sup>2</sup>-D<sup>3</sup> in i+1 and i+2 position of the β turn and L<sup>5</sup> in the central position of an (inverse) γ turn. The strategy seems also to be applicable to C5a, since the C-terminal-derived C5a antagonist NMe-Phe-Lys-Pro-D-Cha-Trp-D-Arg (Cha: cyclohexylalanine)

shows a well defined structure in solution in which the lysine sidechain is in close proximity to the D-arginine carboxylate. Ring closure resulted in a backbone-to-sidechain cyclized peptide, *cyclo*-Ac-Phe-(Orn-Pro-D-Cha-Trp-D-Arg-) (brackets indicate the sidechain-to-backbone mode of cyclization, Orn-NH<sup>E</sup>-CO-D-Arg) with an IC<sub>50</sub> value of 9.28 μM for the displacement of [<sup>125</sup>I]C5a from human polymorph nuclear (PMN) cells. Conformational analysis revealed a γ turn with Pro in the central position stabilized by a hydrogen bond between the flanking amino acids, Orn-CO<sup>E</sup>HN-D-Cha, together with a "pseudo" βII turn involving D-Cha-Trp-D-Arg-Orn defined by a second hydrogen bond between D-Cha-CO<sup>E</sup>HN-Orn. This is consistent with φ<sub>i+1</sub>/ψ<sub>i+1</sub> and φ<sub>i+2</sub>/ψ<sub>i+2</sub> dihedrals of Trp and D-Arg (-58°/90°; 69°/-3°) confirming a β turn type II (ideal values: -60°/120°; 80°/0°) arrangement [295]. More detailed SAR studies showed that the L-Arg containing isomer is much more active than the D-Arg congener (IC<sub>50</sub>=20 nM; inhibition of C5a-induced release of myeloperoxidase from PMNs). The NMR-derived solution structure reveals an inverse γ turn (γ<sub>i</sub>) involving D-Cha-Trp-Arg stabilized by a hydrogen bond between D-Cha-CO<sup>E</sup>HN-Arg [296].

## CONCLUSION

This review was intended to highlight not only the relevance of the GPCR superfamily for drug development purposes during the last decade, but also the tremendous potential of that particular target class for future medicinal chemistry programs aimed to uncover new ligands for peptide-binding GPCRs. Especially the cross-fertilizing combination of ligand-derived structure rationales with the dramatically enhanced efficiency of automated synthesis and combinatorial chemistry will enable pharmaceutical research to identify new chemical entities more rapidly. Even though we have witnessed a technology-based quantum leap forward in efficiency within medicinal chemistry in the late 1990's, the vigorous search for novel GPCR genes within e.g. the human genome has far outpaced the identification of novel endogenous and exogenous ligands. The identification of these ligands remains one of the most challenging tasks in modern pharmacology. The number of GPCRs for which endogenous or exogenous ligands are unknown today continues to increase, thus offering modern pharmaceutical research new opportunities in that entirely new drug targets associated with innovative therapeutic principles emerge. In this context, new low-molecular weight ligands for these orphan receptors will undoubtedly lead to novel insights into the complexity of numerous poorly understood human disorders. Consequently, targeted medicinal chemistry approaches towards members of the GPCR family will facilitate the understanding of the precise physiological role of orphan receptors as well as produce new compounds as qualified lead structures for clinical development.

Concluding, the field of GPCR research is clearly expected to grow dramatically due to the progress that will be made in the human genome initiative, demanding increased contributions from medicinal chemistry in order to provide new pharmacological tools as well as new leads for the development of new drugs.

## ACKNOWLEDGEMENT

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**Paracel BLAST Results**

MEGABLAST 1.2.3-Paracel [2001-11-20]

**Reference:**

Zheng Zhang, Scott Schwartz, Lukas Wagner, and Webb Miller (2000),  
"A greedy algorithm for aligning DNA sequences",  
J Comput Biol 2000; 7(1-2):203-14.

**Database:** Homo\_sapiens.latestgp.masked.fa  
44,521 sequences; 200,768,834,160 total letters

**Query=** hGPR\_29  
(942 letters)

Sequences producing significant alignments:	Score (bits)	E Value
AL133267.9.1.44788	1859	0.0
AC093007.4.37303.78590	547	e-153
Z98744.2.1.100374	547	e-153
AL022727.1.1.144868	105	5e-20

>AL133267.9.1.44788  
Length = 44788

Score = 1859 bits (938), Expect = 0.0  
Identities = 941/942 (99%)  
Strand = Plus / Plus

Query: 1 atgaattggtaaatgacagcatcatacaggagttattctgtctgggttctcagatcg 60  
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 20708 atgaattggtaaatgacagcatcatacaggagttattctgtctgggttctcagatcg 20767

Query: 61 ccttggctggagttccactccttgtggcttcttgatttcttacactgtgaccatctt 120  
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 20768 ccttggctggagttccactccttgtggcttcttgatttcttacactgtgaccatctt 20827

Query: 121 ggcaatctgaccattattcttagtgtcacgcctggacaccaaacttcataccccatgtat 180  
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 20828 ggcaatctgaccattattcttagtgtcacgcctggacaccaaacttcataccccatgtat 20887

Query: 181 tttttcttaccaatctatcactcctggatcttgcacaccatgtacagtcccacaa 240  
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 20888 tttttcttaccaatctatcactcctggatcttgcacaccatgtacagtcccacaa 20947

Query: 241 atgcttagtaaatttatgcagcatcaggaaagtaatcagttatcgtggctgttagccag 300  
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 20948 atgcttagtaaatttatgcagcatcaggaaagtaatcagttatcgtggctgttagccag 21007

Query: 301 ctttcatattctggccttggggctactgaatatcttcctggccgtatgcctt 360  
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 21008 ctttcatattctggccttggggctactgaatatcttcctggccgtatgcctt 21067

Query: 361 gatagggtttagctattgtcgccctccattactcagttatcatgcaccagagactc 420  
Sbjct: 21068 gatagggtttagctattgtcgccctccattactcagttatcatgcaccagagactc 21127

Query: 421 tgcctccagttggcagccgatcctgggtactggtttagtaactcagtggttgtct 480  
Sbjct: 21128 tgcctccagttggcagctgcacccctgggtactggtttagtaactcagtggttgtct 21187

Query: 481 accctgactctccagctgccactctgtgacccctatgtgatagatcacttctctgtgaa 540  
Sbjct: 21188 accctgactctccagctgccactctgtgacccctatgtgatagatcacttctctgtgaa 21247

Query: 541 gtccctgcaactgctcaagttatcttgtgttagacaacacagcaaatgaggctgaactattc 600  
Sbjct: 21248 gtccctgcaactgctcaagttatcttgtgttagacaacacagcaaatgaggctgaactattc 21307

Query: 601 cttgtcagttagtgcatttcataataccctgacactcatccttatcatatgcttt 660  
Sbjct: 21308 cttgtcagttagtgcatttcataataccctgacactcatccttatcatatgcttt 21367

Query: 661 attgtccgagcagtattgaggatacagtcgtgaaggcgacaaaaagcattggaca 720  
Sbjct: 21368 attgtccgagcagtattgaggatacagtcgtgaaggcgacaaaaagcattggaca 21427

Query: 721 tgtggttccatctaattgtgggtctttttatagtagcagccgtctgtgtacctg 780  
Sbjct: 21428 tgtggttccatctaattgtgggtctttttatagtagcagccgtctgtgtacctg 21487

Query: 781 caaccacccatgcggccagctccaaggaccaaggaaagatggttctcttatgaaatc 840  
Sbjct: 21488 caaccacccatgcggccagctccaaggaccaaggaaagatggttctcttatgaaatc 21547

Query: 841 attgcacccatgctgaatcccattatatacacttaggaacaaggaggtaaggaaaggc 900  
Sbjct: 21548 attgcacccatgctgaatcccattatatacacttaggaacaaggaggtaaggaaaggc 21607

Query: 901 ttaaaagggttgggtcaagagtcttcttaatcaagaaataa 942  
Sbjct: 21608 ttaaaagggttgggtcaagagtcttcttaatcaagaaataa 21649

>AC093007.4.37303.78590  
Length = 41288

Score = 547 bits (276), Expect = e-153  
Identities = 387/423 (91%), Gaps = 5/423 (1%)  
Strand = Plus / Minus

Query: 523 gatcaacttgc-tctgtgaagtccctgcaactgctcaagttatcttgcgttggacaacagc 581  
Sbjct: 36552 gatcac-ttcttcgtgaagtccctgctcgctcaagttgcgttggacaacagc 36494

Query: 582 aaatgaggctgaactattcctt-gtcagtggcttccatctaataccctgacactca 640  
Sbjct: 36493 aaatgaggctgaactatt-cttcatcagtgtgctattccttctaataccctgacactca 36435

Query: 641 tccttatatcatatgctttattgtccgaggcgttggatacgtctgctgaaggc 700  
Sbjct: 36434 tccttatatcgatgctttattgtccaaggcgttggatacgtctgctgaaggc 36375

Query: 701 gacaaaaaggcatttgggacatgtggccatctaattgtgggtctctttttatagta 760  
Sbjct: 36374 aacgaaaggcatttgggacatgtggccatctaattgtgggtcactttttatggta 36315

Query: 761 cagccgtctctgtgtacctgcaaccacccatcgcccagctccaaaggaccaaggaaatgg 820  
Sbjct: 36314 cagctatctccatgtacctgcaaccacccatcgcccagctccaaaggacccggggaaatgg 36255

Query: 821 tttctcttttatgttggatcatgtgcacccatgtgaatcccttatataacttagga 880  
Sbjct: 36254 tttctctttctgttggatcatgtgcacccatgtgaatcccttatataacttagga 36195

Query: 881 acaaggaggtaaaggaaaggctttaaaagggttgtgcaa-gagtcttcttaatcaagaaa 939  
Sbjct: 36194 acaaagaggtaaaggaaaggctttaaaagggttgtgcaaagagtgcttcttaatcaagaaa 36135

Query: 940 taa 942  
Sbjct: 36134 taa 36132

Score = 377 bits (190), Expect = e-102  
Identities = 404/474 (85%), Gaps = 8/474 (1%)  
Strand = Plus / Minus

Query: 1 atgaattggtaaatgacagcatcatacaggagttattctgtctgggtttctcagatcga 60  
Sbjct: 37074 atgaattggtaataagagtgtcccacaggagttcattctgttagtttctcagatcaa 37015

Query: 61 ccttggctggagttccactcctt-gtggtctt-ctgatttcttaca-ctgtgaccatc 117  
Sbjct: 37014 ccatggctagagattccac-ccttgcgtatgttct-gtttcttatatct-tgacaatc 36958

Query: 118 tttggcaatctgaccattattctagtgtcacgcctggacaccaaacttcataccccatg 177  
Sbjct: 36957 tttggcaatctgacaataattcttgcgtcacatgtggatttcaaactccacacccatg 36898

Query: 178 tatttttttcttaccaatctatcactccctggatcttgttacaccacatgtacagttcca 237  
|| || || || || || || || || || || || || || || || || || || || || || || || ||  
Sbjct: 36897 tacttttttcttagcaatcttcactccctggaccttgcataaccacaagtacagttcca 36838

Query: 238 caaatgcttagtaaaatttatgcagcatcaggaaagtaatcagttatcgtggctgttagcc 297  
Sbjct: 36837 caaatgctggtaaacatatatgcacaccaggaaagtaatcagttatggtggtggcc 36778

Query: 298 cagctttcatattc-tggcctggggctactgaatatcttcctggccgtatgtc 356  
Sbjct: 36777 cagctttcat-ttgcctggcctgggttccacagaatgtcttcctggccgtatgtg 36719

Query: 357 ct~~t~~gtatagg~~t~~ttgtagctattgtcg~~gg~~c~~t~~tc~~c~~attactcagttatcatgcacc~~a~~gag 416  
Sbjct: 36718 ct~~t~~gtatagg~~t~~ttgtagctattgtcg~~gg~~c~~t~~tc~~c~~attactcaattatcatgcacc~~a~~gag 36659

Query: 417 actctgcctccagttggcagccgcacatcctgggttactggtttagtaactcagt 470  
Sbjct: 36658 gctctgcctccagttggcagtcgcacatcctggatttagtggtttagcaattcagt 36605

>Z98744.2.1.100374  
Length = 100374

Score = 547 bits (276), Expect = e-153  
Identities = 387/423 (91%), Gaps = 5/423 (1%)  
Strand = Plus / Minus

Query: 523 gatcaacttgc-tctgtgaagtccctgcaactgctcaagttatcttgcgttgagacaacacgc 581  
Sbjct: 75538 gatcac-tttctctgtgaagtccctgctgctcaagttgtcctgtgttgacacaacacgc 75480

Query: 582 aaatgaggctgaactattcctt-gtcagtgagcttccatctaataccctgacactca 640  
Sbjct: 75479 aaatgaggctgaactatt-cttcatcagtgctattcttctaataccctgacactca 75421

Query: 641 tccttatatcatatgtttattgtccgagcagtattgaggatacagtctgctgaaggtc 700  
Sbjct: 75420 tccttatatcgtagtgcgtttattgtccaagcagtgttgagaatccagtctgctgaaggtc 75361

Query: 701 gacaaaaagcatttggacatgtggttccatctaattgtggtgtctttttatagta 760  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Sbjct: 75360 aacgaaaggcatttggacatgtggctccatctaattgtggtgtactttttatggta 75301

Query: 761 cagccgtctctgtgtacctgcaaccacccatcgcccagctccaaggaccaggaaagatgg 820  
Sbjct: 75300 cagcttatctccatgtacctgcaaccacccatcgcccagctccaaggaccggggaaagatgg 75241

Query: 821 tttctcttttatggaatcattgcacccatgctgaatccccttatataacttagga 880  
Sbjct: 75240 tttctctttctgtgaatcattgcacccatgctgaatccccttatataacttagga 75181

Query: 881 acaaggaggtaaaggaaggcttaaaagggttgtgcaa-gagtcttcttaatcaagaaa 939  
Sbjct: 75180 acaaagaggtaaaggaaggcttaaaagggttgtgcaaagagtcttcttaatcaagaaa 75121

Query: 940 taa 942  
Sbjct: 75120 taa 75118

Score = 377 bits (190), Expect = e-102  
Identities = 405/475 (85%), Gaps = 10/475 (2%)  
Strand = Plus / Minus

Query: 1 atgaattggtaaatgacagcatcatacaggagttattctgctgggttcagatcg 60  
Sbjct: 76060 atgaattggtaataagagtgtcccacaggagttcattctgttagtttcagatcaa 76001

Query: 61 ctttggctggagttccactcc-ttgtg--gtcttcttgatttctaca-ctgtgaccat 116  
Sbjct: 76000 ccatggctagagattccac-cctttgtatgt-ttc-tgtttcttatatct-tgacaat 75945

Query: 117 ctttggcaatctgaccattattctagtgtcacgcctggacaccaaacttcataccccat 176  
Sbjct: 75944 ctttggcaatctgacaataattctgtgtcacatgtggattcaaactccacacccat 75885

Query: 177 gtattttttcttaccatatctatcactcctggatcttggataccacatgtacagtccc 236  
Sbjct: 75884 gtactttttcttagcaatctcactcctggaccttgcataaccacaagtacagtcc 75825

Query: 237 acaaatgcttagtaatttatgcagcatcaggaaagtaatcagttatcggtgtgttagc 296  
Sbjct: 75824 acaaatgctggtaaacatatgcaacaccaggaaagtaatcagttatgggtgtgtggc 75765

Query: 297 ccagctttcatattt-ctggcctggggctactgaatatcttcctggccgtcatgt 355  
Sbjct: 75764 ccagctttcat-tttctggcctgggttccacagaatgtcttcctggccgtcatgt 75706

Query: 356 ccttgatagttttagctattgtcgccctccattactcagttatcatgcaccaga 415  
Sbjct: 75705 gcttgatagttttagctattgtcgccctccattactcaattatcatgcaccaga 75646

Query: 416 gactctgcctccagttggcagccgatcctgggttactggtttagtaactcagt 470  
Sbjct: 75645 ggctctgcttcagttggcagctgcattcctggattgtggcttagcaattcagt 75591

&gt;AL022727.1.1.144868

Length = 144868

Score = 105 bits (53), Expect = 5e-20

Identities = 126/150 (84%), Gaps = 2/150 (1%)

Strand = Plus / Minus

Query: 694 gaaggctcgacaaaaagcattgggacatgtgggtccatc-taattgtggtgtcttt 752

||||||| || || || || || || || || || || || || || || || || || || || || ||

Sbjct: 7874 gaaggacggcaaaaagcattgggacatgtgggtccca-catgattgtggtgtcccttt 7816

Query: 753 ttatagtacagccgtctctgtgtacacctgcaaccacccctcgcccaaggctccaaggccaagg 812

||||| | || || || | | || || || || || || || || || || || || || || || ||

Sbjct: 7815 ttatgaaacagccatttatatatgtatcttcaaccacccatccacctctaaggactgggg 7756

Query: 813 aaagatggttctcttcttatggaatcat 842

||||||| || || || || || || || || || || || || || || || || || || ||

Sbjct: 7755 aaagatggttccctttcttatggaatcat 7726

Database: Homo\_sapiens.latestgp.masked.fa

Posted date: Jan 4, 2003 2:12 PM

Number of letters in database: 200,768,834,160

Number of sequences in database: 44,521

Lambda	K	H
1.37	0.711	1.31

Gapped

Lambda	K	H
1.37	0.711	1.31

Matrix: blastn matrix:1 -3

Gap Penalties: Existence: 0, Extension: 0

Number of Hits to DB: 0

length of query: 1886

length of database: 200,768,834,160

effective HSP length: 22

effective length of query: 920

effective search space used: 0

T: 0

A: 0

X1: 0 ( 0.0 bits)

X2: 20 (39.6 bits)

S1: 12 (24.3 bits)

S2: 38 (75.8 bits)